

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 15:07:39 ; Search time 765 Seconds
(without alignments)

7052.564 Million cell updates/sec

Title: US-09-914-220B-2

Sequence: 1 gaagaagtcgaagggtctctt.....atgaagaagggttcaactta 1270

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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7: geneseq2003as:*
8: geneseq2003bs:*
9: geneseq2003cs:*
10: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195.6	94.1	1349	3 AAC37629	Aac37629 Arabidops
2	1171.6	92.3	1317	3 AAC46130	Aac46130 Arabidops
3	440.6	34.7	3999	3 AAA71993	Aa71993 A. thaliana
4	154	12.1	281	7 ABX88982	ABX88982 Corn ear-
5	126.6	10.0	968	6 ABN98523	ABN98523 Arabidops
6	57.2	4.5	623	4 AAS25522	Aas25522 Human ova
7	57.2	4.5	1812	9 ADE84891	Ade84891 Farnesyl
8	56.8	4.5	1380	7 ABX13847	ABX13847 DNA encod
9	56.8	4.5	1903	3 AAF21640	Aaf21640 Human bre
10	56.8	4.5	2156	6 ABK84110	ABK84110 Human bre
11	56.8	4.5	2156	6 ACC50146	Acc50146 Breast ca
12	56.8	4.5	2157	2 AAV24010	Aav24010 Human FK5
13	56.8	4.5	2246	6 ABZ35317	Abz35317 Human gen
14	51.4	4.0	2070	2 AAQ48515	Aaq48515 Encodes r
15	50.4	4.0	2000	7 ADA71938	Ada71938 Rice gene
16	47.4	3.7	1055	3 AAC50803	Aac50803 Arabidops
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18	47.2	3.7	110000	5 AAI61373_0	Aai61373 Soybean 3
19	46.4	3.7	618	4 AAS24140	Aas24140 Human ova
20	46.4	3.7	618	5 AAH82715	Aah82715 Human ova
21	45.8	3.6	405	9 ADB75900	Adb75900 Tomato pl
22	45.8	3.6	1057	3 AAC35414	Aac35414 Arabidops
23	45	3.5	2000	7 ADA71938	Ada71938 Rice gene

24	44	3.5	1374	8 ADA02578	Ada02578 Human FXB
25	44	3.5	1374	9 ADB72316	Adb72316 Human FXB
26	44	3.5	1619	2 AAT18796	Aat18796 Human imm
27	44	3.5	1694	8 ADA02577	Ada02577 Human FXB
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31	44	3.5	2291	7 ACA64936	Aca64936 Human FXB
32	44	3.5	2291	9 ADB31398	Adb31398 Testoster
33	44	3.5	3109	3 AAC78150	Aac78150 Human can
34	44	3.5	3954	7 ACA03923	Aca03923 cDNA down
35	44	3.5	3954	10 ADE76909	Ade76909 Human cDN
36	43.4	3.4	1492	4 ABL07819	AbL07819 Drosophila
37	42.4	3.3	542	6 ABK63251	Abk63251 Rat seque
38	42.4	3.3	542	9 ADB57513	Adb57513 Toxicity-
39	42.4	3.3	542	9 ADB52033	Adb52033 Primary r
40	42.2	3.3	892	3 AAC44787	Aac44787 Zea mays
41	42.2	3.3	110000	2 AAX20248_00	Aax20248 Botrellia
42	40	3.1	315	4 AAI24342	Aai24342 Probe #14
43	40	3.1	315	4 ABA69479	Aba69479 Human foe
44	40	3.1	315	4 AAI49610	Aai49610 Probe #18
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ALIGNMENTS

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KW	Hybridisation assay; genetic mapping; gene expression control;
KM	protein identification; signal transduction pathway; metabolic pathway;
KM	promoter; termination sequence; ss.
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OS	Arabidopsis thaliana.
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FD	06-SEP-2000.
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RESULT 2
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ID AAC46130 standard; DNA, 1317 BP.
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AC AAC46130;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49012.
XX
KW Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
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PR 21-JUL-1999; 99US-015086P.
PR 21-JUL-1999; 99US-015088P.
PR 22-JUL-1999; 99US-015085P.
PR 22-JUL-1999; 99US-015087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.

PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-014591P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 03-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
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PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151103P.
PR 31-AUG-1999; 99US-015138P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153707P.
PR 11-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154779P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-015717P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.

FT		/tag= j
FT		/number= 5
FT	intron	3273. .3412
FT		/tag= k
FT		/number= 5
FT	exon	3413. .3565
FT		/tag= l
FT		/number= 6
FT	intron	3566. .3654
FT		/tag= m
FT		/number= 6
FT	exon	3655. .3987
FT		/tag= n
FT		/number= 7
XX		
PN	DEI907598-A1.	
XX		
PD	24-AUG-2000.	
XX		
PF	22-FEB-1999; 99DE-01007598.	
PR	22-FEB-1999; 99DE-01007598.	
XX		
PA	(SCHU/) SCHULZ B.	
XX		
DR	WPI; 2000-566218/53.	
XX	P-PSDB; AAB10674.	
PT	New DNA encoding plant FK506-binding protein analog useful for producing	
PT	transgenic plants with altered architecture and for studying	
PT	immunosuppressants.	
XX		
PS	Claim 1; Page 10-13; 14pp; German.	
XX		
CC	This invention describes a novel DNA sequence (I) containing the coding	
CC	region for an FKBP (FK506-binding protein)-like twisted dwarf protein	
CC	(II) of Arabidopsis thaliana which has plant growth regulating activity.	
CC	(I) or their fragments and derivatives) are used for transforming	
CC	prokaryotic or eukaryotic cells, homologous recombination or for	
CC	expression of a non-translated RNA that, by antisense, co-suppression or	
CC	ribozyme activity, inhibits one or more endogenous FKBP-like genes in a	
CC	cell, altering the response of plants to brassinosteroids (or their	
CC	precursors or derivatives) and their signal transduction and reception,	
CC	for altering ethylene-induced gravitropic reactions in roots or ethylene-	
CC	mediated signal transduction of the gravitropic stimulus and for altering	
CC	the extension growth and growth orientation of plants to change plant	
CC	architecture. Also (I) can be used to identify related sequences in other	
CC	plants by hybridization under low stringency conditions or by polymerase	
CC	chain reaction (PCR), and to generate transgenic plants that are useful	
CC	for studying the activity and signal-transduction processes of	
CC	immunosuppressants (e.g. FK506, cyclosporin A, rapamycin and related	
CC	compounds). This sequence encodes the Arabidopsis thaliana FKBP twisted	
CC	dwarf protein which is described in the method of the invention	
XX		
SQ	Sequence 3999 BP; 1189 A; 697 C; 845 G; 1268 T; 0 U; 0 Other;	
Query Match	34.7%; Score 440.6; DB 3; Length 3999;	
Best Local Similarity	69.6%; Pred. No. 3.6e-118;	
Matches 822; Conservative 0; Mismatches 19; Indels 340; Gaps 3;		
OY	419 TGAGCAGCAACCTTATGTAATTGGTTCTTGAAAAAGAAAAGAACAATGACCGGTTTAGC 478	
Db	2819 TGTGCACATCAAGAGTGAATAATGTTGTCGTGAGCACAGAAAAAAGAACTTAGCGGTTTAGC 2878	
OY	479 CATGGATGTTGCTAGCATGAAGTCGTGGAACGTGCGTGTGCAATGTGGCTGGGAATT 538	
Db	2879 CATGGATGTTGCTAGCATGAAGTCGTGGAACGTGCGTGTGCAATGTGGCTGGGAATT 2938	
OY	539 AGCTTATGGAGAAAGAGAACTTTCTTTTCCAAATGTTCCACTTATGGAGAGACTTGT 598	
Db	2939 AGCTTATGGAGAAAGAGAACTTTCTTTTCCAAATGTTCCACTTATGGAGAGACTTGT 2998	
OY	599 ATATGAGTGAAGTATTGGGTTTGATGAACAAG----- 636	

Db	2299	ATATGAGTGGAACTTATTGGTTTGATGAAACAAAGAGTAAGTATTTCCTATCA	3058
OY	637	-----	636
Db	3059	TCATCTTGTTCTTACCAGACGACTCCATCCAGCTTATCCCACTCTTGCTT	3118
OY	637	-----AGGAAAAGCTCGAGTATATGACTGTAGA	667
Db	3119	ACCTCTGACTTAGATGATGTATTGAACAGGAAAAGCTCGAGTATATGACTGTAGA	3178
OY	668	GGAAGATTGGTGCACAGACAGAGAAAAATGATGGAAATCTCTTTTAAAGAGA	727
Db	3179	GGAAAGATTGGTGCACAGACAGAAAAATGATGGAAATCTCTTTTAAAGAGA	3238
OY	728	GAAACTGAGAGACCATGCACAGTATGAAAT-----	760
Db	3239	GAACTGAGAGAGACCATGCACAGTATGAAATGTTATGCAATCTCTCTATCTATAC	3298
OY	761	-----	760
Db	3299	TCTCTTTTCAACAAATTACGGTCAAAAGTTTAGTTTCAGGCATATCTTAGAGACTGCTC	3358
OY	761	-----GGCCATA	767
Db	3359	GAGGCTCTGTGTTCTTTCGGCTTTTGATGTACATGTTTTGCTGTTTCAGGCATAT	3418
OY	768	GCATATCATGGGGAGCGATTTTATGTTTTACGCTGTATGGGAAGTACAGATATATGGCTTTA	827
Db	3419	GCATATCATGGGGAGCGATTTTATGTTTTACGCTGTATGGGAAGTACAGATATATGGCTTTA	3478
OY	828	GCATTTAAAAAACCATGCCATCTTAAACATAGCAGCTTCCCTCATGCAACCTTAAACGATAC	887
Db	3479	GCATTTAAAAAACCATGCCATCTTAAACATAGCAGCTTCCCTCATGCAACCTTAAACGATAC	3538
OY	888	GATAGACAATTGGTCACTGCAACAT-----	914
Db	3539	GATAGACAATTGGTCACTGCAACATTTGTAAAGCATCATCAACCATTCATTTGAAGAAA	3598
OY	915	-----GTGT	918
Db	3599	TCATTAAAGTTCATACTCGGTTTCTCGAAATCTAATCAAACTCAAACTTATCAGGTGT	3658
OY	919	TGACAGAAAGAGAAAAAACCAGAACGACTGTTCAAGAGGGAAGCAAGGACAGAC	978
Db	3659	TGACAGAAAGAGAAAAAACCAGAACGACTGTTCAAGAGGGAAGCAAGGACAGAC	3718
OY	979	TAGACAGATGGACTGCAGACGTGTATTTCCGAAAGGCAAAAAGTATAGCTCTGACG	1038
Db	3719	TAGACAGATGGACTGCAGACGTGTATTTCCGAAAGGCAAAAAGTATAGCTCTGACG	3778
OY	1039	ACAAGGCGATTTAGAAAGAGCTACGAGCACTTGCAGAGCAAGAGAAAAGCTTTGACCAA	1098
Db	3779	ACAAGGCGATTTAGAAAGAGCTACGAGCACTTGCAGAGCAAGAGAAAAGCTTTGACCAA	3838
OY	1099	AGCAGAAAGAAATGTACAAAGAAATATTCAAGGGAAGATGAAGGTGTCTAGTCAA	1158
Db	3839	AGCAGAAAGAAATGTACAAAGAAATATTCAAGGGAAGATGAAGGTGTCTAGTCAA	3898
OY	1159	AGACCTTTTTTGGTTGATAGTGTATTAGGGAATGGTTTGTCCCTTTCTCCCGATATCT	1218
Db	3899	AGACCTTTTTTGGTTGATAGTGTATTAGGGAATGGTTTGTCCCTTTCTCCCGATATCT	3958
OY	1219	TTTCAGCCCAACAGAGTTAAAGCAGATTAATGTATGAAGAAG	1259
Db	3959	TTTCAGCCCAACAGAGTTAAAGCAGATTAATGTATGAAGAAG	3999
RESULT 4			
ABX88982			
1D	ABX88982 standard; cDNA; 281 BP.		
AC	ABX88982;		

Db 424 AAGGACAGAAAGATTAAGAGAGCATATATCAAAAATGTTGCTTAGAAGGATT 483
 QY 1142 AGGTGCTGCTTAAGT 1155
 Db 484 CAGTTTGGCTTATT 497

RESULT 7
 ID ADE84891 standard; DNA; 1812 BP.
 AC ADE84891;
 XX 29-JAN-2004 (first entry)

DE Farnesyl transferase inhibitor modulated leukemia associated gene #110.
 KM 88; cytostatic; farnesyl transferase inhibitor; gene expression;
 KM quinolone; leukemia; cancer.
 OS Homo sapiens.
 PN WC2003038129-A2.
 PD 08-MAY-2003.
 PF 30-OCT-2002; 2002W0-US034784.
 PR 30-OCT-2001; 2001US-0338997P.
 PR 30-OCT-2001; 2001US-034081P.
 PR 30-OCT-2001; 2001US-0340938P.
 PR 30-OCT-2001; 2001US-0341012P.

(ORTH) ORTHO CLINICAL DIAGNOSTICS INC.

PI Rapam M;
 DR WPI; 2003-513497/48.

PT Determining whether a patient will respond to treatment with a farnesyl
 PT transferase inhibitor, by analyzing the expression of gene that is
 PT differentially modulated in the presence of the inhibitor.

PS Disclosure; SEQ ID NO 110; 346bp; English.

XX The invention relates to a method of determining whether a patient will
 CC respond to treatment with a farnesyl transferase inhibitor (FTI), by
 CC analyzing the expression of gene that is differentially modulated in the
 CC presence of an FTI. The method is useful for determining whether a
 CC patient will respond to treatment with a FTI such as (B)-6-(amino(4-
 CC chlorophenyl)-(1-methyl-1H-imidazol-5-yl)methyl)-4-(3-chlorophenyl)-1-
 CC methyl-2-(1H)quinoline, monitoring the therapy of a patient, treating a
 CC patient with leukemia with FTI if the analysis indicates that the patient
 CC will respond. This sequence corresponds to a gene whose expression may be
 CC modulated in the presence of FTI.

XX Sequence 1812 BP; 550 A; 335 C; 433 G; 493 T; 0 U; 1 Other;

Query Match 4.5%; Score 57.2; DB 9; Length 1812;
 Best Local Similarity 46.2%; Pred. No. 7.6e-06;
 Matches 228; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

QY 662 TGTGAGGAAAGATTGCTGACAGACAGAAAGAAATGAGGAAATCTCTTTTAA 721
 Db 744 TGTGAGAAATTTATTAATTAACAGAAAGCTTAAACATTTGAAATCTTTTCAA 803
 QY 722 GAGAGAAATGAGGAAAGGATGCAAGATGAAATGAGGCAATGAGGAGGAG 781
 Db 804 ATCCCAAGACTGGAGATGCTTATTAATAAATATGCGAACTTTTAAATAC--GTGGA 860
 QY 782 CGATTATATGTTTACGCTGATGGAAGTACAGAGATATGCTTTAGCAGTTAAAAA 841
 Db 861 CAGTTCAAAGGCTGTATTGAGACAGAGATAGAGCAAGCTGCAACCTTAGCTTTAAG 920

QY 842 AAGCATCTTAACATGACGCTTGCCTCATCAAACTTAACATGATGAGCAATTGG 901
 Db 921 CTGTGATCTGAATATGATGCTGTAACTGAAGATGTCAAAATGGCAGGCAATTGA 980
 QY 902 TCACGTCAACATTTGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 961
 Db 981 CAGTTGTTTGAAGGCTCTTGAATCAAGACCATCAAAATACAAAGATTTGATCGGAGAG 1040
 QY 962 GAAAGCAAGGAG 1021
 Db 1041 TCAAGATGAGCAAGATTAAGAGATATGATCAAGCATTTGGCTGATCTTAAGAGAGCTCA 1100
 QY 1022 AAGTATGCTCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081
 Db 1101 GGGATATGACACAGAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1160
 QY 1082 GAAAGCTTTGTACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1141
 Db 1161 AAGGACAGAAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1220
 QY 1142 AGGTGCTGCTTAAGT 1155
 Db 1221 CAGTTTGGCTTATT 1234

RESULT 8

ABX13847
 ID ABX13847 standard; DNA; 1380 BP.
 XX
 AC ABX13847;
 XX
 DT 25-FEB-2003 (first entry)

DE DNA encoding monoclonal antibody preparation method related protein #3.
 XX
 DE Transformation; antibody; peptidyl prolyl isomerase; PPIase; human;
 KM chaperone-like activity; monoclonal antibody preparation; gene; ds.

OS Homo sapiens.

XX Location/Qualifiers
 FT 1..1380
 FT CDS
 FT /*tag= a
 FT /product= "Monoclonal antibody preparation method related
 FT protein #3"

JP2002262883-A.

17-SEP-2002.

13-MAR-2001; 2001JP-00070928.

13-MAR-2001; 2001JP-00070928.

(SEKI) SEKISUI CHEM IND CO LTD.

(KAITO) KAITO BIOTECHNOLOGY KENKYUSHO KK.

WPI; 2003-132125/13.

P-PDB; ABG72858.

A transformant useful for preparing a monoclonal antibody comprises an

antibody gene and a gene encoding PPIase.

Disclosure; Page 14; 16pp; Japanese.

The invention describes a transformant containing an antibody gene and a
 CC gene encoding a peptidyl prolyl isomerase (PPIase) having chaperone-like
 CC activity. The methods detailed using the transformant are useful for the
 CC preparation of a monoclonal antibody. This sequence encodes a protein
 CC associated with the method of preparing a monoclonal antibody described
 CC in the invention

XX

SQ Sequence 1380 BP; 388 A; 318 C; 414 G; 260 T; 0 U; 0 Other;
Query Match 4.5%; Score 56.8; DB 7; Length 1380;
Best Local Similarity 47.5%; Pred. No. 8.7e-06;
Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;
QY 471 GGTTCAGCCATCGGTGTTGCTAGCATGAAGCTGTGTGCTGCTTGTGCTATGTTGGC 530
DB 607 GGTCTGAGAGGGCCATTCAGCGCATGAGAGAAAGAAACATTCATCGTACTCAAG 666
QY 531 TGGGAATTAGCTTATGGAAGAAAGAAACTTTTCTTTCCCAATGTTCCACTATGCA 590
DB 667 CCCAGCATATGCTTTTGGCAGGTGGGAGGAAAAAGTT---CCAAATCCCAACCAATGCT 723
QY 591 GACTGTATATGAGGTGGAAGTATTGGGTTTGATGAAACAAAGAGGGGAAAAAGCTCGC 650
DB 724 GAGCTGAAATATGATTAATACCTCAAGAGTTTGAAGGCGCAAGAG-----TCT 774
QY 651 AGTATATGACTGTAGAGAAAGGATTGTGCACAGACAGAAAGAAAAATGATGGGAAT 710
DB 775 TGGGAGATGATTCAGAAAGAGAGCTGGAACAGACACCATATGTAAGAAAGCGGGCAGCT 834
QY 711 TCTCTTTTAAAGAGGAAAGAACTGGAGAGCCATGCAACATGTGAATGGCCATAGCA 770
DB 835 GTGTACTTCAAGAGAGGTAATACAAACAGCTTTACTAGATTAAGAAATGCTGTCT 894
QY 771 TACATGGGGAGCAATTTATGTTTACCTGTATGGAAGTACAGATATGGCTTTAGCA 830
DB 895 TGGCTGAATATGATGCTAGTCTT-----TCCATAGAGAGAGACAGAAAGCAGGCC 948
QY 831 GTTAAAAACCATGCTCTTAACTAGACAGCTTGCCTCATCAAACTTAAACGATAGAT 890
DB 949 CTTCGACTGGGCTCTCACTCACTCACTGCGCATGTGTATGTGAAACTAGAGGCTTCTCT 1008
QY 891 GAAGCAATTGTCTACTGCAACATTTGTGTGACAGAAAGAGAAAAACCAAGAGCAGT 950
DB 1009 GCTGCCATTGAAAGCTGTAAACAGGCCCTAGAACTGACAGCAACAGAAAGGGCTC 1068
QY 951 TTCAAGAGAGGAAAGCAAGGAGCAGAGCTAGGACAGATGAGCTCAGACGCTGATTTTC 1010
DB 1069 TTCCGCGGGAGAGAGGCCACCTGGCCGTGAATACCTTTGAACTGGGAGCGGCTGATTTTC 1128
QY 1011 CGAAAGGACAAAAGTATGCTCTGACAGCAAGGCGATTAGAAAGAGCT 1060
DB 1129 CAGAAAGTCTGACAGCTCTACCCCAACAAAGAGCCGCCAAGACCCAGCT 1178
RESULT 9
AAF21640
ID AAF21640 standard; DNA; 1903 BP.
XX
AC AAF21640;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human breast and ovarian cancer associated antigen gene SEQ ID 27.
XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiviral; vulnery; anticonvulsant;
KW antifungal; antifungal; antiparasitic; cardiac; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease; ds.
XX
OS Homo sapiens.
XX
PN WO200055173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005881.

XX
PR 12-MAR-1999; 99US-0124270P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-611515/58.
XX
DR P-PDB; AAB58737.
PT New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention, treatment
PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
PT neurological diseases.
XX
PS Claim 1; Page 501; 1299pp; English.
XX
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive; neurotropic;
CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
CC antiinflammatory; antiviral; antiparasitic; cardiac; anticonvulsant;
CC antifungal; antiparasitic and cardiac activity. The polynucleotide and
CC protein sequences are used in the diagnosis of cancer, particularly
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
CC and agonists may also be used in the diagnosis, prevention and treatment
CC of immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC cardiovascular disorders such as myocardial ischaemias; wound healing;
CC neurological diseases such as cerebral anoxia and epilepsy; and
CC infectious diseases
XX
SQ Sequence 1903 BP; 478 A; 470 C; 528 G; 427 T; 0 U; 0 Other;
Query Match 4.5%; Score 56.8; DB 3; Length 1903;
Best Local Similarity 47.5%; Pred. No. 1e-05; Indels 18; Gaps 3;
Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;
QY 471 GGTTCAGCCATCGGTGTTGCTAGCATGAAGCTGTGTGAGCGCTTGTGCTATGTTGGC 530
DB 446 GGTCTGAGAGGGCCATTCAGCGCATGAGAGAAAGAAACATTCATCGTACTCAAG 505
QY 531 TGGGAATTAGCTTATGGAAGAAAGAACTTTCTTTTCCCAATGTTCCACTATGCA 590
DB 506 CCCAGCTATGCTTTTGGCAGGTGGGAGGAAAGTT---CCAAATCCCAACCAATGCT 562
QY 591 GACTGTATATGAGGTGGAAGTATTGGGTTTGATGAAACAAAGAGGGGAAAAAGCTCGC 650
DB 563 GAGCTGAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 613
QY 651 AGTATATGACTGTAGAGAAAGATTTGTGACAGACAGAAAGAAATGATGGGAAT 710
DB 614 TGGGAGATGATTCAGAAAGAGAGCTGGAACAGAGACATATGTAAGAGCGGGCAGCT 673
QY 711 TCTCTTTTAAAGAGGAAAGAACTGGAGAAAGCCATGCAACATGTGAATGGCCATAGCA 770
DB 674 GTGTACTTCAAGAGAGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 733
QY 771 TACATGGGGAGCAATTTATGTTTACGCTGTATGGAAGTATACAGATATGCTTTAGCA 830
DB 734 TGGCTGAATATGATGCTAGTCTT-----TCCATAGAGAGAGACAGAAAGCAGGCC 787
QY 831 GTTAAAAACCATGCTCTTAACTAGACAGCTTGCCTCATCAAACTTAAACGATAGAT 890
DB 788 CTTCGACTGGGCTCTCACTCACTCACTGCGCATGTGTATGTGAATCAAGGCTTCTCT 847
QY 891 GAAGCAATTGTCTACTGCAACATTTGTGTGACAGAAAGAGAAAAACCAAGAGCAGT 950

Db	848	GGTGGCATTGAAGAGCTGTAAACAAGGCCCTTAAAGACTGGAACAGCAACAACGAAGAAGGCCCTC	907
Oy	951	TTGAGAAAGAGGAAAGCAAAAGGCAGAGCTTAGAGACAGATGAGACTCAGCAGCTGATGATTTTC	101
Db	908	TTCCCGCCGGGGGAGAGGCCCACTGGCCCTGTAATGATCTTGAACCTGGCACGGGCTGATTTTC	967
Oy	1011	CGAAAGGCGCAAAAGATGATGCTCTGACGCAAGAGCGCATTTAGAAAGAGCT	1060
Db	968	CAGAAAGTCTCTGAGCTTACTCCCAACAACAAAGCCGCCAAGCCAGCT	1017
RESULT	10		
ID	ABK84110		
AC	ABK84110	standard; cDNA; 2156 BP.	
XX	ABK84110;		
DT	14-AUG-2002	(first entry)	
DE	Human	cDNA differentially expressed in granulocytic cells #681.	
XX	Human; BS; granulocytic cell; DNA chip; bacterial infection;		
KW	viral infection; parasitic infection; protozoal infection;		
KW	fungal infection; sterile inflammatory disease; psoriasis;		
KM	rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;		
KW	cardiac reperfusion injury; renal reperfusion injury; ARDS;		
KW	adult respiratory distress syndrome; inflammatory bowel disease;		
KW	Crohn's disease; ulcerative colitis; periodontal disease;		
KV	granulocyte activation; chronic inflammation; allergy.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200228999-A2.		
XX			
PD	11-APR-2002.		
XX			
PF	03-OCT-2001; 2001MO-US030821.		
XX			
PR	03-OCT-2000; 2000US-0237189P.		
XX			
PA	(GENE-) GENE LOGIC INC.		
XX			
PI	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;		
XX			
DR	WP1; 2002-435328/46.		
XX			
PT	Detecting granulocyte activation by detecting differential expression of		
PT	genes associated with granulocyte activation, which serves as diagnostic		
PT	markers that is useful for monitoring disease states and drug toxicity.		
PS	Claim 1; SEQ ID NO 681; 114pp; English.		
XX			
XX	The invention relates to detecting (M1) granulocyte (GC) activation		
CC	(GCA), by detecting the level of expression of gene(s) (Gs) identified by		
CC	DNA chip analysis as given in the specification, and comparing the		
CC	expression level to an expression level in an unactivated GC, where		
CC	differential expression of Gs is indicative of GCA. Also included are		
CC	modulating (M2) GA by contacting GC with an agent that alters the		
CC	expression of at least one gene in Gs; (2) screening (M3) for an agent		
CC	capable of modulating GCA or an inflammation (especially chronic) in a		
CC	tissue, an allergic response in a subject, exposure of a subject to a		
CC	pathogen or sterile inflammatory disease using the gene expression		
CC	profile; (3) detecting (M4) an inflammation (especially chronic) in a		
CC	tissue, an allergic response in a subject, exposure of a subject to a		
CC	pathogen or sterile inflammatory disease, by detecting the level of		
CC	expression in a sample of the tissue of gene(s) from Gs, where the level		
CC	of expression of the gene is indicative of inflammation; (4) treating		
CC	(M5) an inflammation (especially chronic) or in a tissue, an allergic		
CC	response in a subject, exposure of a subject to a pathogen or sterile		
CC	inflammatory disease, by contacting a tissue having inflammation with an		
CC	agent that modulates the expression of gene(s) from Gs in the tissue. M1		
CC	is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful		
CC	for screening an agent capable of modulating GCA preferably in an		

[illegible]

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XX Homo sapiens.
OS
XX WO2003004989-A2.
XX
XX 16-JAN-2003.
XX
XX 21-JUN-2002; 2002WO-US019669.
XX
XX 21-JUN-2001; 2001US-0299887P.
XX
XX 27-JUN-2001; 2001US-0301572P.
XX
XX 18-JUL-2001; 2001US-0306501P.
XX
XX 25-SEP-2001; 2001US-0325002P.
XX
XX 05-MAR-2002; 2002US-0362585P.
XX
XX 14-MAY-2002; 2002US-0380391P.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX Lillie J, Gannavarapu M, Glatk K, Hoerh S, Kamatkar S;
XX Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
XX Best RC, Hortobagyi GN, Puzeta L, Meric F, Sahin A, Mills GB;
XX WPI; 2003-210381/20.
XX P-PSDB; ABR47454.
XX
XX Breast cancer diagnosis or treatment by comparing the level of expression
XX of a marker in a patient sample with that in the control non-breast
XX cancer sample.
XX
XX Claim 1; SEQ ID NO 139; 128bp; English.
XX
XX The present invention describes a method for assessing whether a patient
XX is afflicted with breast cancer. The method comprises comparing the level
XX of expression of a marker (gene/polypeptide see ACC50076 to ACC5034 and
XX ABR47386 to ABR47632) in a patient sample and the normal level of
XX expression of the marker in a control non-breast cancer sample, where a
XX significant increase in the level of expression of the marker in the
XX patient sample and the normal level is an indication that the patient is
XX afflicted with breast cancer. The breast cancer associated sequences from
XX the present invention have cytostatic activities and can be used in gene
XX therapy. The method is useful for diagnosing and treating breast cancer.
XX C. N. B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2156 BP; 530 A; 551 C; 606 G; 469 T; 0 U; 0 Other;
XX
XX Query Match 4.5%; Score 56.8; DB 7; Length 2156;
XX Best Local Similarity 47.5%; Pred. No. 1.1e-05;
XX Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;
XX
XX 471 GGTTCACCATCGGTGTTGCTAGCATGAAGTCTGCTGAGAGTGGCTTGTCATGTTGGC 530
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 706 GGTCTGAGAGGGGCATTCAGCCGATGAGAGAAAGCAATTCATCGTACCTCAAG 765
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 531 TGGGAATTAAGCTATGAGGAAAGAGAAAGCAATTTCTTTCCCAATGTTCCACCTATGCA 590
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 766 CCCAGCTATGCTTTGGCAGTGTGGAGAGAAAAGTT---CCAAATCCCAACCAATGCT 822
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 591 GACTTGTATATGAGGTGAGAGTATTTGGGTTTGATGAAACAAAGAGGAGAAAAGCTGCG 650
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 823 GAGCTGAATATGAAATTAACCTCAAGAGTTTGAAGGCAAGGAGGAGGAGGAGGAGGAGG 873
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 651 AGTATATGACTGATGAGAGAAAGATGTTGTCAGACACACAGAGAGAGAGAGAGAGAGAT 710
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 874 TGGAGATGATTAAGAGAGAAAGTGAAGCAAGCAACCAATGTTGAAGAGAGAGAGAGAGCT 933
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 711 TCTCTTTTAAAGAGAGAGAAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 770
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 934 GTGACTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 993
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 771 TACATGGGGAGAGATTTTATGTTTCACTGTATGAGAGAGATGATGCTTTAGCA 830
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 994 TGGCTGAATATGAGTCTAGTATTT-----TCCATATGAGAGAGACAGAGAGAGAGGCC 1047
Qy 831 GTTAAAGAACCCATGCATCTTAACATAGAGCTGCTGCTCAATAAAGATATAGAT 890
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1048 CTTCGACTGACCTCTCACTCAACCTGCGCATGTGTGATCTGAACTACAGGCTTCTCT 1107
Qy 891 GAAGCAATTTGTCATCTGCAACATTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCTG 950
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1108 GCTGCAATTTGAAGAGCTGTAAACAGAGGCCCTAGAACTGAGACAGACAGACAGAGAGAGGCTTC 1167
Qy 951 TTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 1010
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1168 TTCGCGCGGAGAGAGGCCCACTGCGCGGAGATGACTTTGAACTGCGCAGGCGGTGATTTTC 1227
Qy 1011 CGAAGAGCAAAAGATGCTCTGACGAGCAAGAGCGATTTAGAGAGAGCT 1060
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1228 CAGAGAGTCTCTGAGCTTACCCCAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGCT 1277

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10266

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RESULT 12
AAV24010
ID AAV24010 standard; DNA; 2157 BP.
XX
XX AAV24010;
XX
XX 06-AUG-1998 (first entry)
XX
XX Human FK506 binding protein, FKBP52, coding sequence.
XX
XX FK506 binding protein; FKBP52; human; immune response regulator;
XX immunosuppressant; steroid hormone receptor transformation; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 100..1479
XX FT /*tag= a
XX FT /product= "FKBP52"
XX
XX PN US5763590-A.
XX
XX PD 09-JUN-1998.
XX
XX PF 09-NOV-1994; 94US-00336618.
XX
XX PR 11-OCT-1991; 91US-00777752.
XX
XX PR 16-OCT-1992; 92US-00963325.
XX
XX PR 29-MAR-1994; 94US-00218989.
XX
XX PA (VERT-) VERTEX PHARM INC.
XX
XX PI Peattie DA, Livingston DJ, Harding MW;
XX
XX DR WPI; 1998-347419/30.
XX
XX P-PSDB; AAM54038.
XX
XX DNA sequence encoding human FK506-binding protein - and recombinant DNA
XX molecule containing it.
XX
XX Claim 1; Fig 3; 28bp; English.
XX
XX This sequence encodes 52 kD human FK506 binding protein, referred to as
XX FKBP52, of the invention. The FKBP52 protein plays a key role in
XX regulating immune responses. FKBP52 may be useful for mediating steroid
XX hormone receptor transformation. The DNA may be used to screen for new
XX immunosuppressants, and in assays for metabolites in samples from
XX individuals taking immunosuppressants. The DNA may also be used in assays
XX for identifying natural intracellular rapamycin-like or FK506 like
XX substances, and in assays for identifying natural intracellular
XX substrates that are potential targets for other immunosuppressants
XX
XX Sequence 2157 BP; 531 A; 551 C; 606 G; 469 T; 0 U; 0 Other;
XX

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Query Match 4.5%; Score 56.8; DB 2; Length 2157;
 Best Local Similarity 47.5%; Pred. No. 1.1e-05;
 Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GGTAAACCATCGGTGTTGCTAGCATGAAGCTCTGTAAAGCTGGCTTGTGCATGTTGGC 530
 DB 706 GGTGTGAGAGGGGCGATTCAGCGCATGAGAAAGAAACATTCATCGTGTACTCAAG 765

QY 531 TGGGAATTAAGCTTATGGAAGAAAGAAACCTTTCTTTCCCAATGTTCACCTATGCA 590
 DB 766 CCCAGCATATGCTTTTGGCAGGTGTTGGAGAGAAAGTT---CCAAATCCCAACCAATGCT 822

QY 591 GACTTGTATATGAGGTGGAAGTTATGCGTGTGATGAAACAAAGAGAGGAAAGCTGCG 650
 DB 823 GAGCTGAATATGATTAACCTCAAGAGTTTGAAGAGGCAAGG-----TCT 873

QY 651 AGTATATGACTGTAGAGAAAGATTTGGTGCACAGACAGAGAAATATGATGGAAAT 710
 DB 874 TGGGAGATGAATTCAGAAAGAAAGCTGGAACAGACACATAGTGAAGAGCGGGGCACT 933

QY 711 TCTCTTTTAAAGAGAGAAACCTGAGAGAGCCATGCAAGATATGATGATGCA 770
 DB 934 GTGTACTTCAAGAGAGTAAATACAGCAAGCTTACTACAGATATAGAAAGATGTCT 993

QY 771 TACATGGGAGAGCAATTTATGTTTCACTGTATGGAAGTACAGATATGCTTTAGCA 830
 DB 994 TGGCTGAATATGAGTCTAGTTT-----TCCAATGAGAAAGCAAGAAAGCAGGCC 1047

QY 831 GTTAAAAACCATGCGCATCTTAACATGACAGCTTGCCTCATCAACTTAAACGATACAT 890
 DB 1048 CTTGACTGCGCTCTCACTCACTCACTGCGCATGATGTATGTGAATCAACGAGGCTTCTCT 1107

QY 891 GAAGCAATTTGATCACTGCAACATTTGTGTGAACAGAAAGAAACCCAAAGACACTG 950
 DB 1108 GCTGCCATTGAAGCTTTAACHAGGCCCTTGAATCTGACAGCAACCAAGAGGGCTTC 1167

QY 951 TTCAAGAGAGGAAAGCAAGGCAAGCTAGACAGATGACCTCAAGCGTGAATTC 1010
 DB 1168 TTCGCGCGGGAGAGGCCCACTGGCGGTGAATGACTTTGAACCTGCAACGGGCTGATTC 1227

QY 1011 CGAAAGGCAAAAAGTATGCTCTGACGACAGGCGATTTGAAGAGCT 1060
 DB 1228 CAGAAAGTCTCTGACGCTCTACCCCAACAAAGAGCCGCCAAGCCAGCT 1277

RESULT 13
 ABZ35317
 ID ABZ35317 standard; cDNA; 2246 BP.
 AC ABZ35317;
 XX
 DT 05-FEB-2003 (first entry)
 XX
 DE Human gene expression profile polynucleotide SEQ ID NO 428.
 XX
 DE Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
 XX bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
 XX tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
 XX gene expression; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200274979-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-MAR-2002; 2002MO-US008456.
 XX
 PR 20-MAR-2001; 2001US-0276947P.
 XX (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 PA
 XX
 PI Wan J, Wang Y;

XX
 DR WPI; 2002-740862/80.
 XX
 PT New gene expression profile generated from primary, endothelial,
 PT epithelial, and muscle cell types, useful for identifying disease
 PT pathologies involving alterations of gene expression, e.g. cancer.
 XX
 PS Example 3; Page 575-576; 850pp; English.

XX
 CC The invention relates to a gene expression profile comprising one or more
 CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
 CC endothelium, myometrium microvascular endothelium, keratinocyte
 CC epithelium, bronchial epithelium, mammary epithelium, prostate
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
 CC small airway epithelium, renal epithelium, umbilical artery smooth
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
 CC osteoblasts or prostate stromal cell. The gene expression profile is used
 CC for determining the level of RNA expression for a sample, determining the
 CC phenotype of a cell and distinguishing cell types. The gene or a protein
 CC expression profile is useful in identifying disease pathologies involving
 CC alterations of gene expression. The assessment of expression profiles may
 CC provide meaningful information with respect to tumour type and stage.
 CC treatment methods, and prognosis. The gene or protein expression profile
 CC may also be used for creating microarrays. The microarray is useful for
 CC genetic and physical mapping of genomes, DNA sequencing, genetic or
 CC medical diagnosis, genotyping of organisms, confirming cell or tissue
 CC identifications and in identifying promising antibiotics, antiviral or
 CC antifungal agents

SQ
 Sequence 2246 BP; 547 A; 580 C; 632 G; 487 T; 0 U; 0 Other;

Query Match 4.5%; Score 56.8; DB 6; Length 2246;
 Best Local Similarity 47.5%; Pred. No. 1.1e-05;
 Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GGTAAACCATCGGTGTTGCTAGCATGAAGCTCTGTAAAGCTGGCTTGTGCATGTTGGC 530
 DB 762 GGTCTGAGAGGGCCATTAAGCGCATGAGAAAGAAACATTCATCGTGTACTCAAG 821

QY 531 TGGGAATTAAGCTTATGGAAGAAAGAAACCTTTCTTTCCCAATGTTCCACTATGCA 590
 DB 822 CCCAGCATATGCTTTTGGCAGGTGTTGGAGAGAAAGTT---CCAAATCCCAACCAATGCT 878

QY 591 GACTTGTATATGAGGTGGAAGTTATGCGTGTGATGAAACAAAGAGGGAAGAGCTCGC 650
 DB 879 GAGCTGAATATGATTAACCTCAAGAGTTTGAAGAGCCAAAGGAG-----TCT 929

QY 651 AGTATATGACTGTAGAGAAAGATTTGTGACAGACAGAGAAAGAAATGATGGAAAT 710
 DB 930 TGGGAGATGAATTCABAAGAGAGCTGGAAGAGACATATGTAAGAGGGGCACT 989

QY 711 TCTCTTTTAAAGAGAGAACTGAGAGAACCATGCAACATGATGAATGGCATAGCA 770
 DB 990 GTGTACTTCAAGAGAGTAAATACAGCAAGCTTTACTACAGTATGAAGATCGGTCT 1049

QY 771 TACATGGGAGAGATTTTATGTTTCACTGTATGGAAGTATCAAGATATGCTTTAGCA 830
 DB 1050 TGGCTGAATATGAGTCTAGTTT-----TCCAATGAGAGAGCAAGAAAGCAGGCC 1103

QY 831 GTTAAAAACCATGCGCATCTTAACATGACAGCTTGCCTCATCAACTTAAAGATAGAT 890
 DB 1104 CTTGACGTGCGCTCTCACTCAACCTGCGCATGTGTCATGTAACCTCAAGGCTTCTCT 1163

QY 891 GAAGCAATTTGTCACTGCAACATTTGTGTCAGAGAAAGAGAAACCCAAAGAGACTG 950
 DB 1164 GCTGCATTTGAAGAGCTGTAAAGAGGCCCTTGAAGCTGACAGCAACCAAGAGGGCTTC 1223

QY 951 TTCAAGAGAGGGAAGCAAGGCAAGGATGAGACAGATGAGCTCAAGCATGATATGATTC 1010

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Db      1224 TTCCGCGCGGAGAGGCCCACTGCGCGCTGATGACCTTTGAACCTGCGACCGGCTGATTTTC 1283
QY      1011 CGAAGGCAACAAAAGTATGCTCTCTGACGACAGGCGATTGGAAGAGCT 1060
Db      1284 CAGAAAGTCTCTGACGCTCTACCCCAACAAGCCGCCCAAGACCCAGCT 1333

RESULT 14
AAQ48515
ID      AAQ48515 standard; cDNA; 2070 BP.
XX
XX      AAQ48515;
AC
XX      25-MAR-2003 (revised)
DT      28-MAR-1994 (first entry)
XX
XX      Encodes rabbit HBI protein which binds hsp90.
DE
XX      steroid hormone receptor; immunosuppressor; FK506; binding protein; FKBP;
KM      heat shock protein; hsp90; chaperone protein; rotamase activity; ss.
XX
XX      Oryctolagus cuniculus.
XX
XX      Key
FH      4.1380
FT      CDS
FT      /*tag= a
FT      /product= "HBI"
XX
XX      WO9318146-A2.
XX
XX      16-SEP-1993.
XX
XX      04-MAR-1993; 93WO-FR000219.
XX
XX      04-MAR-1992; 92FR-00002612.
XX
XX      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA
XX      Lebeau M, Massol N, Renoir M, Radanyi C, Mornon J, Callebaut I;
PI      Baillet E, Chambraud B;
XX
XX      WPI; 1993-303460/38.
DR      P-PSDB; AAR41781.
XX
XX      New protein forming complex with heat shock protein - also binding immuno
PT      -suppressors, etc., and corresp. nucleic acid antibodies etc., useful
PT      e.g. for detecting tumours, treating auto-immune disease, etc.
XX
XX      Claim 1; Fig 1; 43pp; French.
PS
XX      The HBI protein is able to complex chaperone protein hsp90, even when the
CC      chaperone protein is part of a hetero-oligomer with other proteins. Hsp90
CC      can bind to steroid hormone receptors, vitamin D, and Tyrosine Kinases of
CC      viral oncogenes; HBI is thus useful for the study, prevention or
CC      treatment of diseases associated with dysfunction of proteins which form
CC      complexes with hsp90, e.g. rickets, cancer, dioxin poisoning or
CC      autoimmune disease. HBI can also be used in immunosuppressor research.
CC      The cDNA sequence coding for HBI was isolated by screening a rabbit liver
CC      cDNA library with a probe based on part of a protein known to be present
CC      in a steroid receptor complex. (Updated on 25-MAR-2003 to correct PN
CC      field.)
XX
XX      Sequence 2070 BP; 480 A; 549 C; 620 G; 421 T; 0 U; 0 Other;
SQ
XX

Query Match      4.0%; Score 51.4; DB 2; Length 2070;
Best Local Similarity 46.8%; Pred. No. 0.00041;
Matches 200; Conservative 0; Mismatches 221; Indels 6; Gaps 1;
QY      634 AGAAGGCAACAAAAGTCTCTGACGCTCTGATGACCTTTGGAAGGATTGGTGCAGACAGAGAA 693
Db      761 AGAAGGCAACAAAAGTCTCTGAGATGAGCTCGAGAGAGAAAGCTGAGACAGAGCCCACTCG 820

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QY      694 GAAAAATGATGGGAATTCCTTTTAAAGAGAGAAACTGGAGAGGCAATGCAACACT 753
Db      821 TGAAGAAGGAGGCAACGTGTACTTCAAGAAAGCAAGTAAACAAGGAGGCTGTGTACAGT 880
QY      754 ATGAATGGCCATGATGATCATGAGGAGAGCAATTTATGTTTCAAGCTGTATGGAAAGTACC 813
Db      881 ACAAGAAGATTGTGTTTGTGCTGGGAATACGAATCAAGTTTT-----TCCAGTGAAGGAAG 934
QY      814 AGGATATGCTTTAGACGTTTAAAAAACCATGCGATCTTAAACATAGCAGGCTTCCATCA 873
Db      935 TGCATAAAGGACAGAGGCGCTGCGCGCTGCGCTCCCACTCAACCTGGGTATGTGACCTGA 994
QY      874 AACTAAACAGATACGATGGAAGCAATTGTCTACTGCAACATTTGTTGACAGAAAGAGA 933
Db      995 AGCTACAGGCTTTCTGCGCAGCGGTGGAAGCTGTAAACAAGGCCCTGGAACCTGGAACAGA 1054
QY      934 AAAACCAAAAGCAGCTGTTTCAAGAAAGGGAAGCAAAAGGACAGAGCTAGACAGATGAGACT 993
Db      1055 ACAACGAGAAAGGCGCTTTCGCGCGGGAAGGCCCACTGCGTGTGAACGACTTTGACC 1114
QY      994 CAGCAGTGATGATTTCCGAAAGGCACAAAGATGCTGCTGACGACAGGCGATTAGAA 1053
Db      1115 TGGACAGGCTGACTTTCAGAAAGTCTTGCAAGCTTACCCAGCAACAAAGCGGCTAAG 1174
QY      1054 GAGAGCT 1060
Db      1175 CCCAGCT 1181

RESULT 15
ADA71938
ID      ADA71938 standard; DNA; 2000 BP.
XX
XX      ADA71938;
AC
XX      20-NOV-2003 (first entry)
DT
XX
XX      Rice gene, SEQ ID 5263.
DE
XX
XX      Plant; bacterial infection; fungal infection; viral infection; rice;
KM      gene; ds.
XX
XX      Oryza sativa.
OS
XX
XX      WO2003000898-A1.
PN
XX      03-JAN-2003.
PD
XX      22-JUN-2001; 2001WO-IB001105.
PF
XX      22-JUN-2001; 2001WO-IB001105.
PR
XX      22-JUN-2001; 2001WO-IB001105.
PS
XX      (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX      Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX      Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
PI      WPI; 2003-175290/17.
XX
XX      Identifying at least one gene involved in plant resistance or response to
PT      pathogenic infection for conferring resistance or tolerance to a plant to
PT      bacterial, fungal or viral infection by determining or detecting plant
PT      gene expression.
XX
XX      Claim 27; SEQ ID NO 5263; 899pp; English.
PS
XX
XX      The present invention relates to a method (M1) for identifying genes
CC      involved in plant resistance or response to pathogenic infection. M1
CC      comprises identifying a gene whose expression is significantly altered in
CC      the incompatible interaction of plant gene expression relative to
CC      expression of the gene in an uninfected plant, in a mutant plant that
CC      does not express a gene associated with response to pathogenic infection,
CC      or in a corresponding incompatible or compatible interaction. (M1) is

```

CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX
SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 4.0%; Score 50.4; DB 7; Length 2000;

Best Local Similarity 9.6%; Pred. No. 0.00078;

Matches 66; Conservative 310; Mismatches 301; Indels 11; Gaps 1;

```
QY 478 CCATGGGTGTTGATGATGAAGTCTGTGAACGCGCTTGATGATGCTGGGAAT 537
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 MMRSMCRMSKACCYMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMRMR 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 538 TAGCTTATGGAAGAAAGAACTTTCTTTCCCAATGTTCCACTATGACAGACTTGT 597
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 SCKRARMMKRCRSGRAMKRCGCMCRMSYGMWRMSWRMSKRYKMSRMRYMRKK 467
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 598 TATATGAGTGAAGTATTTGATTTGATGAACAAGAGAGAAAGCTGCAGTGATA 657
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 468 CSRTTMMGKTRGMMGTMRGRYKRSKMRKRRMRMRMRMRMRMRMRMRMRMR 527
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 658 TGACTGTAGAGAAAGATTTGTCAGACAGACAGAAAGAAATGATGGAATTCCTTT 717
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 ARKYSYSAARKACWYRGKYWAGMMWKYKMYKMYKMYKMYKMYKMYKMYKMY 587
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 718 TTAAGAGAGAAAGCTGAGAGAACCATGCAAGTATGAATGCCATAGCATACATGG 777
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 588 ASCSKSARKAGAKKCKRSKMSKMSKMSKMSKMSKMSKMSKMSKMSKMSKMS 647
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 778 GGGACGATTTTATGTTTCACTGTATGGAAGTACCAAGATATGCTTAGCAGTTAAA 837
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 -----WKSYYTCYMRKMSKMSKSTCTMYTMSKYTAKYSGYRMYRAMCMYMR 696
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 838 ACCCATGCATCTTAACATAGCAGCTTGCTCATCAACTAAAGATAGCATGAGCAA 897
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 697 WYYRYRSYMTYMAWYTSSTRMAMTGMKYSGRYTSWYKCKSMKYRSMWYMSMMWAK 756
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 898 TTGCTCACTGCAACTGTGTGACAGAGAGAGAAAGAAAGCAAAAGCACTGTTCA 957
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 757 TWKMMRRYATRRMMWYRYSKMYTCTMGMGYMMWRYMKRYMKCTKYTWYSAT 816
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 958 GAGGAGAAAGCAAGAGAGAGATGACAGACTGACGATGATTTCCGAAAGG 1017
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 817 YMTGTMAAMMMMAKTKRMGMGTGAKTRBARARATYMKATYCATKRMWTKGAKMA 876
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1018 CACAAAAGTATGCTCTGACGACAAAGCGATTAGAGAGAGCTACGACACTTG 1077
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 877 MAKAMRYKYMSWMAWYYYKYTRRTYKTCWMAKRWGSMWYMRMMWKSAMMMW 936
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 1078 AAGGAAAGCTTTATCAAAAGCAAGAAAGAAATGTACAAAGAAATTTCAAG 1137
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Search completed: July 7, 2004, 16:41:45
Job time : 773 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 15:39:14 ; Search time 8003 Seconds

(without alignments)
6878.127 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270
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Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*
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3: gb_in:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1221.4	96.2	1250	8	AY093009	AY093009 Arabidops
4	1100	86.6	1126	8	BT001192	BT001192 Arabidops
5	529.8	41.7	1142	6	AX034545	AX034545 Sequence
6	518.8	35.6	1396	8	AK065114	AK065114 Oryza sat
7	451.6	35.6	2710	8	ATH224641	AJ224641 Arabidops
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10	229.2	18.0	776	6	AX034547	AX034547 Sequence
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VERSION	AX034542.1				
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SOURCE					
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REFERENCE					
AUTHORS					
JOURNAL	Patent: DE 19907598-A 2 24-AUG-2000;				

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 AJ224640.1 GI:9650630
 VERSION
 KEYWORDS
 FKBP gene.
 SOURCE
 Arabidopsis thaliana (thale cress)
 ORGANISM
 Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
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 1
 Kolkisoglu,U., Berger,J., Eckhoff,A., Moeller,A., Saal,B.,
 Bellini,C. and Schulz,B.
 TITLE
 Structure and evolution of FKBP-1-like genes in Arabidopsis
 JOURNAL
 Unpublished
 AUTHORS
 2 (bases 1 to 1360)
 TITLE
 Direct Submission
 JOURNAL
 Submitted (25-FEB-1998) Schulz B., Max-Delbrueck-Laboratory,
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VERSION AY093009.1 GI:20260219
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SOURCE

Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE

Southwick,A., Karlin-Neumann,G., Nguyen,M., Lam,B., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
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Shinozaki,K., Ecker,D., Theologis,A. and Davis,R.W.

TITLE

Submitted (27-MAR-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

JOURNAL

Direct Submission

COMMENT

e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of the RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA') (Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Southwick,A.,
Nguyen,M., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,
Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
Yamada,K., Ecker,D., Theologis,A. and Davis,R.W.

Southwick,A., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PI.

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QY	867	CTCATCAAACTTAAACGATACAGTAAGAGCAATGGTCACTGCACTATGTTGACAGAA	926
Db	841	CTCATCAAACTTAAACGATACAGTAAGAGCAATGGTCACTGCACTATGTTGACAGAA	900
QY	927	GAAAGAAAAAACCMAAGCACTGTTCAAGAGGGAAAGCAAAAGCAGACTTAGACAG	986
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QY	987	ATGCACTCAGACGCTGATGATTTCCGAAAGGCACAAAGTATGCTCCGACGACAAAGCG	1046
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QY	1227	CACGAGTTAAAGCAGATTATGTTGAAAGAGGTTTCAATT	1269
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RESULT 4

LOCUS DEFINITION	1126 bp	mRNA	linear	PLN 12-NOV-2002
BT001192				
Arabidopsis thaliana FKBP-type peptidyl-prolyl cis-trans isomerases, putative (At3g21640) mRNA, complete cds.				

ACCESSION

VERSION B1001192.1 GI:24899728
KEYWORDS FLI CDNA.

SOURCE

SOURCE Arabidopsis thaliana (thale cress)

ORGANI

ORGANISM *Arabidopsis thaliana*

snematobryta: macron[jon]bryta: eudicotyledons: core eudicots:

rosids: eurosid II: Brassicales: Brassicaceae; Arabidopsis.

REFERENCE

REFERENCE 1 (bases 1 to 1126)

AUTHOR

AUTHORS Tripp, M., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranc

Palm, C.J., Bowser, L., Jones, T., Bahn, J., Carninci, P., Chen, H., Chow, B., Chung, M. K., Hayashizaki, Y., Itohida, J., Kamiya, A.

Kawai, T. : Kim, C. : Lin, J. : Liu, S.-X. : Narusaka, M. : Pham, P.-K. : Cinek, K. : Chuang, M.-K. : Hayashizaki, I. : Ishida, O. : Kamigaya, H. :

Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.

Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.

TITLE

TITLE Direct Submission

JOURNA

JOURNAL
Submitted (12-NOV-2002) DNA sequencing and technology center
Stanford University 855 California Avenue Palo Alto, CA 94304

STANFORD UNIVERSITY, 355 LATHROP AVENUE, 4440 HILL/ ST. 2
USA

COMMENT

COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA': Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Tripp, M., Southwick, A., Nguyen, M., Palm, C.U., Jones, T., Wu, T., Chen, H., Cheu, R., Chan, M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, V. W.

Lee, J.M., Kim, C.J., Quach, H.L., Shim, P., Tang, C.C., Torount, M.,
Wallender, E.K., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S.,
Ecker, J., Theologis, A. and Davis, R.W.

Tripp, M. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.
(SSP/Stanford) contributed equally to this work as PIs.

FEATURES

source

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gene

CDS

ORIGIN

Query Match 86.6%; Score 1100; DB 8; Length 1126;
Best Local Similarity 99.5%; Pred. No. 1.1e-280;

Matches 1114; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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541 AGAAGAAAAATGATGGAATTTCTTTTAAAGAGAGAAATCGAGAGAGCCATGCA 600
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810 TACAGATATGCTTATGAGTAAATAAACCCATGCGATTTAACTAGCAGCTGCGTC 869
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781 GAGAAAAAACCAGAAACGATTTGACAGAGGAAACCAAGGACAGCTAGGACAGATG 840
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1021 TGGTGAATGATGTTATGAGCAATGTTGTTCCCTTTTCCCGTATCTTTCAGAGCGAC 1080
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RESULT 5
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LOCUS AX034545
DEFINITION Sequence 5 from Patent DE19907598.
ACCESSION AX034545
VERSION AX034545.1 GI:10303142
KEYWORDS
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
REFERENCE 1
AUTHORS Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
JOURNAL Patent: DE 19907598-A 5 24-AUG-2000;
SCHULZ BURKHARD (DE)

FEATURES

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ORIGIN

Query Match 41.7%; Score 529.8; DB 6; Length 1142;
Best Local Similarity 73.8%; Pred. No. 2.1e-129;
Matches 686; Conservative 0; Mismatches 242; Indels 1; Gaps 1;
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Db	331	AAAGAAAGCCATGTGTCAGAAAGCCATCAAAATACCAATGCTTTCGTGATTCAGAGCA	390
Qy	378	TGACCAAACTCTGACGACCAAAATTTGAGATTCATGTCATGACGACCAACTATTGAA	437
Db	391	TGGGCTGAAAGACGACGACCAAGTTGAAGATTCATGCGGTAGCAACACCTCTTGAG	450
Qy	438	TTGGTTCTTGGAAAAGAAAAGAACTAGCCCGTTTACCATCCGTTGTGCTAGATG	497
Db	451	CTGGTTATTAAGAAAAGAAAAGAAATATACCTGCTACCTATGCGTTAAACAGATG	510
Qy	498	AAGCTGTGTAACGTGCGCTTGTGTCATGTTGGCTGGAAATTAAGCTTATGAGAAAAGAA	557
Db	511	AAATCCGTTGAGCTGCTTATTTCACTTGTGCTGGAACTAGCTTATGAGAAAAGAA	570
Qy	558	AACTTTCTTTTCCCAATGTTCCACTATGCGACACTTGTATATGAGTGAATTT	617
Db	571	AACTTCTCTTCCCTAATGTCCTCACTACAGCTGATGATGATGATGAGTTGATGAT	630
Qy	618	GGGTTTGATGAAAACAAAGAGGAAAGCTGCGATGATGATGATGATGAGGAAAGAT	677
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Qy	678	GGTGCACAGACAGAAAGAAAATGATGGAATTTCTTTTAAAGAGAGAACTGGAG	737
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Qy	738	GAAGCCATGCAACGATGTAATGTCATGACATACATGCGGACGATTTTATGTTTCA	797
Db	751	GAAGCTATGCAACGATGTAATGTCATGACATACATGCGGACGATTTTATGTTTCA	810
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RESULT 6
 LOCUS AK065114 1396 bp mRNA linear PLN 24-JUL-2003
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J013001006, full insert sequence.
 ACCESSION AK065114
 VERSION AK065114.1 GI:32975132
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE

1 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Komoto, H., Miyazaki, A., Ootomo, Y., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

TITLE

Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

JOURNAL

Science 301 (5631), 376-379 (2003)
 MEDLINE 22752273
 PUBMED 12869764
 JOURNAL 2 (Issues 1 to 1396)

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurihara, C., Kurotaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Nariakawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Ootomo, Y., Ota, Y., Ootomo, Y., Ryu, R., Saiton, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takehashi, F., Takeuchi-Akita, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

TITLE

Submitted (05-DEC-2001) Shoehi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skkuchi@nias.affrc.go.jp, Tel:81-29-858-7007, Fax:81-29-858-7007)

COMMENT

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and Yamamoto, M.
 PAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariakawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,


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Best Local Similarity 69.9%; Pred. No. 1.2e-108;
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LOCUS AX034541
DEFINITION Sequence 1 from Patent DE19907598.
ACCESSION AX034541
VERSION AX034541.1 GI:10303139
KEYWORDS
SOURCE
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
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AUTHORS
JOURNAL
FEATURES
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ORIGIN

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Query Match 35.6%; Score 451.6; DB 6; Length 4010;
Best Local Similarity 69.9%; Pred. No. 1.2e-108;
Matches 833; Conservative 0; Mismatches 19; Indels 340; Gaps 3;
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 VERSION AB019232.1 GI:3869071
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 ORGANISM Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases)
 Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S.
 Structural analysis of Arabidopsis thaliana chromosome 3. I.
 Sequence features of the regions of 4,504,864 bp covered by sixty
 P1 and TAC clones
 DNA Res. 7 (2), 131-135 (2000)
 20277480
 MEDLINE 10819329
 PUBMED 2 (bases 1 to 80818)
 REFERENCE Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asamizu, E. and Tabata, S.
 Direct Submissions
 Submitted (29-OCT-1998) Yasukazu Nakamura, Kazusa DNA Research
 Institute, Department of Plant Gene Research, 1532-3, Yama,
 Kisarazu, Chiba 292-0812, Japan (E-mail: ynakam@kazusa.or.jp,
 Tel:81-438-52-3935, Fax:81-438-52-3934)
 Address for correspondence: kaos@kazusa.or.jp
 For the latest information on annotation of this clone, please see
 http://www.kazusa.or.jp/kaos/cgi-bin/sgd_graph.cgi?c=M1L23
 Genes with similarity to proteins in the databases are described in
 'product' or 'note' qualifiers. Genes that have no significant
 protein similarity are described as 'unknown protein'.
 The software programs used to predict genes include: Gra1
 (Informatics Group, Oak Ridge National Laboratory,
 http://combio.ornl.gov/Gra1-1.3/),
 GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
 NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
 Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
 SplinePredictor (Volker Brendel, Stanford University,
 http://sremlim.zool.iastate.edu/cgi-bin/sp.cgi).
 Genes encoding tRNAs are predicted by tRNAscan-SB
 (Sean Eddy, Washington University School of Medicine, St. Louis,
 http://genome.wustl.edu/eddy/tRNAscan-SB/).
 This sequence may not be the entire insert of this clone. It may be
 shorter because we remove overlaps between neighboring submissions.
 The 5' clone is MHC9 and the 3' clone is MSD21.

FEATURES

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Query Match 35.2%; Score 447.4; DB 8; Length 80818;
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QY 419 TGAGCAGCAACCATTCGATTCCTTGAAAGAGAAAGAAAGAACTAGCCGGTTAGC 478
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	Unknown.		

Segurens,B., Pelleitier,E., Searpelli,C., Salanoubat,M.,
 Weissenbach,J. and Quetier,F.
 Oryza sativa chromosome 12 sequencing
 JOURNAL
 Unpublished
 2 (bases 1 to 125593)
 Genoscope.
 Direct Submission
 Submitted (09-JAN-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 On Oct 17, 2003 this sequence version replaced gi:12329146.
 Center: Genoscope / Centre National de Sequencage
 Center code: GS
 Web site: http://www.genoscope.cns.fr/
 Contact: Segref@genoscope.cns.fr

COMMENT

 The following sequence is oriented from the T7 to the SP6 end.

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 FINISHED SEGMENT ENDS AT BASE 125593

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 9.7%; Score 123.2; DB 8; Length 125593;
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Search completed: July 7, 2004, 18:55:24
 Job time : 8013 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 16:22:54 ; Search time 123 Seconds
(without alignments)
5729.981 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270
Sequence: 1 gaaagtcgaagggctctc.....atgaagaaggttacaatca 1270

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	12.1	281	4	US-09-313-294A-7442
2	71	5.6	7218	1	US-08-232-463-14
3	56.8	4.5	2157	1	US-08-336-618-25
4	56.8	4.5	2246	4	US-09-566-921-48
5	44	3.5	2291	4	US-09-220-132-114
6	40.6	3.2	289	3	US-09-007-005-17
7	40.6	3.2	289	3	US-09-244-796-17
8	39.8	3.1	472	4	US-09-621-976-973
9	37.2	2.9	5252	4	US-09-976-594-308
10	37.2	2.9	5712	4	US-09-976-594-820
11	36.8	2.9	486	3	US-09-358-972-90
12	36.8	2.9	486	4	US-09-406-065-78
13	36.8	2.9	2802	4	US-09-976-594-924
14	36.6	2.9	505	4	US-09-621-976-15639
15	36	2.8	3279	4	US-09-543-681A-2886
16	35.8	2.8	148567	4	US-09-801-876B-3
17	35.8	2.8	148567	4	US-10-254-869-3
18	35.6	2.8	1298	4	US-08-948-705-3
19	35.6	2.8	1298	4	US-09-510-543-3
20	35.4	2.8	1664976	4	US-08-916-421B-1
21	35	2.8	3106	4	US-09-976-594-554
22	34.8	2.7	277	3	US-09-007-005-3
23	34.8	2.7	277	3	US-09-244-796-3
24	34.4	2.7	278	4	US-09-621-976-13872
25	34.4	2.7	603	5	PCT-US92-01691-27
26	34.4	2.7	603	5	PCT-US92-01691-28
27	34.4	2.7	627	4	US-09-833-381-1295

28	34.4	2.7	6519	1	US-08-233-008A-7	Sequence 7, Appl
29	34.4	2.7	10993	4	US-08-961-527-15	Sequence 15, Appl
30	34.2	2.7	3399	4	US-09-621-976-8976	Sequence 8976, Ap
31	34	2.7	1048	2	US-08-897-340-3	Sequence 3, Appl
32	34	2.7	1048	3	US-09-252-329-3	Sequence 3, Appl
33	34	2.7	1756	2	US-08-879-260-3	Sequence 3, Appl
34	34	2.7	1811	3	US-09-231-529-5	Sequence 5, Appl
35	34	2.7	1811	3	US-08-977-816-5	Sequence 5, Appl
36	33.6	2.6	3014	4	US-09-313-294A-7129	Sequence 7129, Ap
37	33.4	2.6	44453	4	US-09-146-053-5	Sequence 5, Appl
38	33.2	2.6	983	3	US-08-960-780-28	Sequence 28, Appl
39	33.2	2.6	983	3	US-09-073-898-28	Sequence 28, Appl
40	33.2	2.6	983	4	US-09-850-351A-28	Sequence 28, Appl
41	33.2	2.6	1069	4	US-09-023-655-166	Sequence 166, Appl
42	33.2	2.6	1194	4	US-08-860-368B-11	Sequence 11, Appl
43	33.2	2.6	1194	3	US-08-860-368B-12	Sequence 12, Appl
44	33.2	2.6	1641	3	US-08-960-780-22	Sequence 22, Appl
45	33.2	2.6	1641	3	US-09-073-898-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-313-294A-7442

Sequence 7442, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Ito, Laura Y.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313, 294A
NUMBER OF SEQ ID NOS: 1999-05-14
SOFTWARE: PERL Program
SEQ ID NO 7442
LENGTH: 281
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Inocyte ID No. 6476212 700381733H1
LOCATION: 235
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7442

Query Match 12.1%; Score 154; DB 4; Length 281;

Best Local Similarity 76.4%; Pred. No. 2.6e-37;
Matches 201; Conservative 0; Mismatches 61; Indels 1; Gaps 1;

QY	642	AAAGCTGCGAGTATGACTGTAGAGAAAGATTGCGACAGACAGAAATAATG	701
DB	2	AAATCCGAGATGACATGACGTTGAAGAGATTGCGACGACAGAAAGATT	61
QY	702	GATGGAAATCTCTTTTAAAGAGAAACTGAGAAACCATGCAAGTATGAATG	761
DB	62	GAGGGCAATCATATTTTCAAGAAAGAGCTTGAAGAGCCATGCAAGTATGAATG	121
QY	762	GCCATGACATACATGCGGAGCATTTTATGTTTCAGCTGATATGGAAGTACGATATG	821
DB	122	GCCATGACATACATGCGGAGCATTTTATGTTTCAGCTGATATGGAAGTACGATATG	181
QY	822	GCTTTGACGTTTAAACCATGCTTAAATGACGCTTGCCTCAATCAATCAATCAAT	881
DB	182	GCTTTGACGTTTAAACCATGCTTAAATGACGCTTGCCTCAATCAATCAATCAAT	240
QY	882	CGATGACATGACGATGCTCA	904
DB	241	AGATTGACATGACGATGCTCA	263

```
RESULT 2
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMTU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZ9pc-F18
; US-08-232-463-14

Query Match          5.6%; Score 71; DB 1; Length 7218;
Best Local Similarity 3.6%; Pred. No. 4,2e-11;
Matches 14; Conservative 236; Mismatches 141; Indels 0; Gaps 0;

QY 601 ATGAGTGAAGTATTGTTGATGATAAAGAGAGAGAAAGCTCGAGTGAATGA 660
    ||| ||| ||| ||| : : : : : : : : : : : : : : : : : : :
DB 1456 AAGAGATAGAAATTTGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1397
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 661 CTGTAGAGAAAGATTGTCAGACAGACAGAAAGAAATGATGGGAATTCCTTTTA 720
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1396 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1337
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 721 AGGAGAGAAAGCTGAGAGAGCATGACAGATGAATGGCATGATACATGGGG 780
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1336 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1277
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 781 ACGATTTATGTTGACCTGTATGGAAGTACAGATATGCTTTAGCATTAAGAAC 840
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1276 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1217
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 841 CAGCCATCTTAACATACAGCTTGCTCATCAAACTAAACATACATGAAGCAATTG 900
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1216 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1157
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 901 GTCACGTCAACATTGTTGACAGAGAGAGAGAAAGCAAGCAGCTGTCAGAGAG 960
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1156 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1097
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 961 GGAAGCAAGAGCAGAGCTAGACAGACATGCA 991
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1096 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRA 1066
    : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
US-08-336-618-25
; Sequence 25, Application US/08336618
; Patent No. 5763590
; GENERAL INFORMATION:
; APPLICANT: Peattie, Debra A.
; APPLICANT: Harding, Matthew W.
; APPLICANT: Livingston, David J.
; TITLE OF INVENTION: ISOLATION OF AN MT 52,000 FK506 BINDING
; TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith and Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,618
; FILING DATE: 09-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,325
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/777,752
; FILING DATE: 11-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: VP191-06A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2157 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100..1476
; US-08-336-618-25

Query Match          4.5%; Score 56.8; DB 1; Length 2157;
Best Local Similarity 4.7.5%; Pred. No. 4.6e-07;
Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;

QY 471 GCTTAGCATGCGTGTGCTAGCATGAAGTCTGTTGAACGCGCTTGATGCTGGC 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 706 GGTCTGAGAGGCGCATTCAGCGCATGAGAGAAAGAGCAATTCATGTTGACTCAAG 765
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Qy 531 TGGGAATTAGCTTATGGGAAGAAGAACTTTTCTTCCCATGTTTCCACCTATGCA 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 766 CCCAGCTATGCTTTGGCAGTGTGGAGAGAAAGTT---CMAATCCCAACCAATGCT 822
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 591 GACTTGTATATGAGGTGGAAGTTATGGGTTTGTATGAAACAAAGAGAGAAAGCTGCG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 823 GAGCTGAATATGATTTACACCTCCAGAGTTTGGAAAGGCCAAGGAG-----TCT 873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 651 AGTGATATGACTGTAGAGAAAGATTGTGACAGACAGAGAAAGAAATGATGGGAT 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 TGGAGATGATTCAGAGAGAAAGCTGGAACAGACCAATGTAAGAAAGAGCGGCGACT 933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 711 TCTCTTTTAAAGAGAGAACTGAGAGCAATGCAAGTATGAAATGGCCATGCA 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 GTGTACTTCAAGAGAGTAAATACAGCAAGCTTTACTACAGTATTAAGAGATGTGCT 993
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 771 TACATGGGAGACGATTTTATGTTTCACTGTATGGAAATACAGATATGCTTTAGCA 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 994 TGGCTGAATATGATGTAGTTT-----TCCAATGAGAGACAGAAAGCAGAGCC 1047
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 831 GTTAAACCCATGCACTTTTACATAGCAGCTTGCTCTCAATCAACTTAAACGATACAT 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1048 CTTGCACTGCTCTCACTCACTCACTGCGCATGTGTATGTGAACCTACAGGCTTCTCT 1107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 891 GAGCAATTGTGCTACATGCAATTTGTGTGACAGAAAGAGAAACCCAAAGCAGCTG 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1108 GTGCCATTGAAAGCTTTAACAGAGCCCTAGAACTGACAGCAACAGAGAGGCGCTC 1167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 951 TTCAAGAGAGAGAAAGCAAGAGCAGAGCTAGACAGATGACCTGACGCTGATGATTC 1010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1168 TTCCGCGGGAGAGAGGCCACCTGCGCGTGAATGACTTTGAACGAGACGGGCTGATTC 1227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1011 CGAAGGACAAAGATATGCTCTGACGACAGAGCGCATTAAGAGAGCT 1060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1228 CAGAGGTCTGTGAGCTCTACCCCAACAGAAAGCCCAAGACCCAGCT 1277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 4
US-09-566-921-48
; Sequence 48, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla W.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 2246
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6682888 474194.5
US-09-566-921-48

```

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Query Match 4.5%; Score 56.8; DB 4; Length 2246;
Best Local Similarity 47.5%; Pred. No. 4.7e-07;
Matches 280; Conservative 0; Mismatches 292; Indels 18; Gaps 3;
Qy 471 GGTATACCATCGGTTGCTAGCATGAGTCTGTAACGTCGCTTGTGCATGTTGGC 530
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 GGTGTGAGAGGCGCATTTACGCGATGAGAAAGAAACCTTCATCGTACTCAAG 821
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 531 TGGGAATTAAGCTTATGGAAGAAAGAACTTTTCTTCCCAATGTTCCACTATGCA 590
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 822 CCCAGCTATGCTTTGGCAGTGTGGAGAGAAAGTT---CMAATCCCAACCAATGCT 878
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 591 GACTTGTATATGAGTGAAGTATGCGTTTGAATGAACAAAGAGAGGAAAGCTGCG 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 879 GAGCTGAATATGATTTACACCTCAAGAGTTTGGAAAGGCCAAGAG-----TCT 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 651 AGTGATATGACTGTAGAGAAAGATTGTGACAGACAGAGAAAGAAATGATGGGAAT 710
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 930 TGGAGATGATTCAGAGAGAAAGCTGGAACAGACCAATGTAAGAAAGAGCGGCGACT 989
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 711 TCTCTTTTAAAGAGAGAACTGAGAGCAATGCAAGTATGAAATGGCCATAGCA 770
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 990 GTGTACTTCAAGAGAGTAAATACAGCAAGCTTTACTACAGTATTAAGAGATGTGCT 1049
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 771 TACATGGGAGACGATTTTATGTTTCACTGTATGGAAATACAGATATGCTTTAGCA 830
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1050 TGGCTGAATATGATGTAGTTT-----TCCAATGAGAGACAGAAAGCAGAGCC 1103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 831 GTTAAACCCATGCACTTTTACATAGCAGCTTGCTCTCAATCAACTTAAACGATACAT 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1104 CTTGCACTGCTCTCACTCACTCACTGCGCATGTGTATGTGAACCTACAGGCTTCTCT 1163
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 891 GAGCAATTGTGCTACATGCAATTTGTGTGACAGAAAGAGAAACCCAAAGCAGCTG 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1164 GTGCCATTGAAAGCTTTAACAGAGCCCTAGAACTGACAGCAACAGAGAGGCGCTC 1223
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 951 TTCAAGAGAGAGAAAGCAAGAGCAGAGCTAGACAGATGAGACTCAGACGCTGATGATTC 1010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1224 TTCCGCGGGAGAGAGGCCACCTGCGCGTGAATGACTTTGAACGAGACGGGCTGATTC 1283
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1011 CGAAGGACAAAGATATGCTCTGACGACAGAGCGCATTAAGAGAGCT 1060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1284 CAGAGGTCTGTGAGCTCTACCCCAACAGAAAGCCCAAGACCCAGCT 1333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 5
US-09-220-132-114
; Sequence 114, Application US/09220132
; Patent No. 650607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANC.
; FILE REFERENCE: 07314-074001
; CURRENT APPLICATION NUMBER: US/09/220,132
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 2291
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-220-132-114

```

```

Query Match 3.5%; Score 44; DB 4; Length 2291;
Best Local Similarity 45.8%; Pred. No. 0.0039;
Matches 281; Conservative 0; Mismatches 315; Indels 18; Gaps 3;
Qy 447 GGAAGAGAGAAAGAAAGCTAGCGGTTTACCATGCGTGTCTGATGAAGTCTGCT 506
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 554 GGAAGAGAGCAAGCACTTCCATTTGGAATTTGCAAGAGCTGTGAGAAATGACGCGGAA 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 507 GAACTGCGCTTGTGATGATGCTGCGAATTAGCTTATGGAAGAGAAAGCTTTTCT 566
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 614 GAACATATGATTTTATATCTTGTGACCAAGTATGTTTGGAGAGCAAGGAGGCTTAA 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 567 TTTCCTCAATGTTTCACTTATGAGCACTGTATATGAGTGAAGTATATGAGTTGAT 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 674 TTGGGCA---TTGAACCTATATGCTGAGCTTATATGAAGTTTACCTTAAGAGCTTCG-- 728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 627 GAAACAAAGAGAGAAAGCTGCACTGATATGACTGTAGAGAGAAAGATTGGTGCAGCA 686
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 729 -----AAAGGCCAAGAATCTGGAGATGATACCAAGAAAATTGGACAGCT 781
Qy 687 GACAGAGAAAATGATGGAAATCTTTTAAAGAGAGAAACTGGAGAAAGCATG 746
Db 782 GCCATTGTCAAGAGAGAGACCGTACTTCAAGGAGCAAAATACATGACAGCGTG 841
Qy 747 CAACAGATGATAATGCGCATAGCATATGAGGAGCATTTTATGTTTACGCTGATGG 806
Db 842 ATTCAATATGGGAAGATAGTGTCTGTTAGAGATGAAATATGTT-----TATCGAA 895
Qy 807 AAGTACCAAGATATGCTTTAGACGTTTAAACCATGTCATTTAATACATGACGCTTC 866
Db 896 AAGGAATCGAAGCTTCTGAATCATTTCTCTGCTCTCTTTCGAACTCGGCGCATGTGC 955
Qy 867 CTATCAACTTAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 926
Db 956 TACTTGAAGCTTAAAGATACCAAGAGCTGTGATGATGATGATGATGATGATGATG 1015
Qy 927 GAAGAGAAAAACCAAGAGCATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 986
Db 1016 GACAGTCCCAATGAGAAAGGCTGTATAGAGAGGAGTGAAGCCGCTGCTCATGAACGAG 1075
Qy 987 ATGACATCAGACGCTGATGATTTCCGAAGGACAAAGTATGCTCTTACGACAGAGCG 1046
Db 1076 TTGAGTCAGCAAGGCTGACTTTGAGAAAGTGTGAGATGAACCCCGAATATAGGCT 1135
Qy 1047 ATTAGAGAGAGCT 1060
Db 1136 GCAGACTGCAGAT 1149

RESULT 6
US-09-007-005-17

; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szoostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007, 005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035, 963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064, 491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match 3.2%, Score 40.6; DB 3; Length 289;
Best Local Similarity 6.2%; Pred. No. 0.013;
Matches 16; Conservative 122; Mismatches 117; Indels 3; Gaps 1;
Qy 907 GCAACATGTGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
Db 9 RCARARURURARURURURURARURURARURURARURURURURURURURURUR 68
Qy 967 CAAGAGCAGAGCTAGACATGACATGACATGACATGACATGACATGACATGAC 1026
Db 69 RNR 128

Qy 1027 ATGCTCTGACAGACAGAGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
Db 129 RNR 188
Qy 1087 CCTTGTAC--CAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1143
Db 189 RNR 248
Qy 1144 GTGCTGCTAAGTCAAGA 1161
Db 249 RNR 266

RESULT 7
US-09-244-796-17

; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szoostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244, 796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035, 963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064, 491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007, 005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match 3.2%, Score 40.6; DB 3; Length 289;
Best Local Similarity 6.2%; Pred. No. 0.013;
Matches 16; Conservative 122; Mismatches 117; Indels 3; Gaps 1;

Qy 907 GCAACATGTGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 966
Db 9 RCARARURURARURURURURARURURARURURARURURURURURURURURUR 68
Qy 967 CAAGAGCAGAGCTAGACATGACATGACATGACATGACATGACATGACATGAC 1026
Db 69 RNR 128
Qy 1027 ATGCTCTGACAGACAGAGGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
Db 129 RNR 188
Qy 1087 CCTTGTAC--CAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1143
Db 189 RNR 248
Qy 1144 GTGCTGCTAAGTCAAGA 1161
Db 249 RNR 266

RESULT 8

US-09-621-976-973
; Sequence 973, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jober, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; PRIORITY FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 973
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..471
US-09-621-976-973

Query Match 3.1%; Score 39.8; DB 4; Length 472;
Best Local Similarity 50.8%; Pred. No. 0.031;
Matches 95; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 158 AATCTCTGAGCATCAAACTCAACACATGACCAAGAGCGAAATGTTACTGAAGGA 217
DB 268 AAGGCCGAGATGAAAAAGCTCCGAAAGAGAGCCAGATGAGTACCGCTGAGTAC 327
QY 218 GTGCGCTTGTGATGATGAGCATCTCAAGAGGGTAAATGTTCTCTAAAGTTATGATGA 277
DB 328 CTGCGGCTGCGCAAGGCGCCAGGCCAGCGTGTAAATGCTGCTATTTGTGATGA 387
QY 278 AGCTGAGCTTGTGATGAGAAAGTCACTAAGCAGATTATTAAGGAAGTCAAGCTTCCAA 337
DB 388 ATGCTGCTGCTTGAAGAAATTTCTTAAGCAAAAGAAAGAGTACTGCTTAAG 447
QY 338 ACCATCC 344
DB 448 AAGCTCC 454

RESULT 9
US-09-976-594-308
; Sequence 308, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976.594
; PRIORITY FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 308
; LENGTH: 5252
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 2619838CBI
US-09-976-594-308

Query Match 2.9%; Score 37.2; DB 4; Length 5252;
Best Local Similarity 51.2%; Pred. No. 0.76; 83; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 870 ATCAAACTAAAGCATGATGAAAGCAATGTCATGCAACATGTTGTGACAGAGAA 929

DB 303 ATCAGAAACAAAGATACAAAGAGCTTTGAAACACTGTATAGACAGTGTAAAGCAAGAG 362
QY 1930 GAGAAACCCAAAGCACTGTTTCAGAAAGGGAAGCAAGAGCTAGACAGATG 989
DB 363 AAAAATATCTATATATGCTCGGGTTTTTATTTGGCGTTCTGCGAGCTGAATCAACCACT 422
QY 990 GACTCAGCAGTATGATTTCCGAAAGGCAAAAGATATGCTCTGACGA 1039
DB 423 GATCAGGCCCAAGTGCTCTATATAAAAGCTGCTGAATTAGACGACGACCA 472

RESULT 10
US-09-976-594-820
; Sequence 820, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976.594
; PRIORITY FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 820
; LENGTH: 5712
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 427967.4
US-09-976-594-820

Query Match 2.9%; Score 37.2; DB 4; Length 5712;
Best Local Similarity 51.2%; Pred. No. 0.8;
Matches 87; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 870 ATCAAACTAAAGCATGATGAAAGCAATGTCATGCAACATGTTGTGACAGAGAA 929
DB 339 ATCAGAAACAAAGATACAAAGAGCTTTGAAACACTGTATAGACAGTGTAAAGCAAGAG 398
QY 930 GAGAAACCCAAAGCACTGTTTCAGAAAGGGAAGCAAGAGCTAGACAGATG 989
DB 399 AAAAATATCTATATATGCTCGGGTTTTTATTTGGCGTTCTGCGAGCTGAATCAACCACT 458
QY 990 GACTCAGCAGTATGATTTCCGAAAGGCAAAAGATATGCTCTGACGA 1039
DB 459 GATCAGGCCCAAGTGCTCTATATAAAAGCTGCTGAATTAGACGACGACCA 508

RESULT 11
US-09-358-972-90
; Sequence 90, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W.
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/358.972
; PRIORITY FILING DATE: 1999-07-22

EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 90
LENGTH: 486
TYPE: DNA
ORGANISM: *Pyrococcus furiosus*
US-09-358-972-90

Query Match 2.9%; Score 36.8; DB 3; Length 486;
Best Local Similarity 56.7%; Pred. No. 0.26;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 653 TGATATGCTGTAGAGAAAGATTGGTCAGCAGACAGAAAGAAATGATGGGAATTC 712
DB 222 TGTATGCTGTAGAGAAAGATTGGTCAGCAGTGAAGTGAAGAAAGATGGCTGAGCTAC 281
QY 713 TCTTTTAAGAGAGAAAGCTGAGAGCCATGCCATGCAATGCAATGCGCATAGCATA 772
DB 282 TGATCCAAAGAGCAGCAGCAGCTGGAGCAATTAGGGGAGATTAGACTTGACATAGGAGA 341

RESULT 12

US-09-406-065-78
Sequence 78, Application US/09406065
Patent No. 6312902
GENERAL INFORMATION:
APPLICANT: Shultz, John W.
APPLICANT: Lewis, Martin K.
APPLICANT: Leippe, Donna
APPLICANT: Mandrekar, Michelle
APPLICANT: Kepnart, Daniel
APPLICANT: Rhodes, Richard B.
APPLICANT: Andrews, Christine A.
APPLICANT: Hartnett, James R.
APPLICANT: Gu, Trent
APPLICANT: Olson, Ryan J.
APPLICANT: Welch, Roy
TITLE OF INVENTION: Improved Nucleic Acid Detection
FILE REFERENCE: Improved Nucleic Acid Detection
CURRENT APPLICATION NUMBER: US/09/406,065
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: 09/358,972
EARLIER FILING DATE: 1999-07-21
EARLIER APPLICATION NUMBER: 09/252,436
EARLIER FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 09/042,287
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 78
LENGTH: 486
TYPE: DNA
ORGANISM: *Pyrococcus furiosus*
US-09-406-065-78

Query Match 2.9%; Score 36.8; DB 4; Length 486;
Best Local Similarity 56.7%; Pred. No. 0.26;
Matches 68; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 653 TGATATGCTGTAGAGAAAGATTGGTCAGCAGACAGAAAGAAATGATGGGAATTC 712
DB 222 TGTATGCTGTAGAGAAAGATTGGTCAGCAGTGAAGTGAAGAAAGATGGCTGAGCTAC 281
QY 713 TCTTTTAAGAGAGAAAGCTGAGAGCCATGCCATGCAATGCAATGCGCATAGCATA 772
DB 282 TGATCCAAAGAGCAGCAGCAGCTGGAGCAATTAGGGGAGATTAGACTTGACATAGGAGA 341

RESULT 13

US-09-976-594-924
Sequence 924, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 924
LENGTH: 2802
TYPE: DNA
ORGANISM: *Homo sapiens*
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 481118.7
LOCATION: 1873, 2029
OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-924

Query Match 2.9%; Score 36.8; DB 4; Length 2802;
Best Local Similarity 47.1%; Pred. No. 0.7; 162; Indels 3; Gaps 1;
Matches 147; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

QY 848 TCTTAACATAGCAGCTTGCCTCATCAACTAAACGATGATGAGCAATTTGTCATG 907
DB 1006 TGTGAAGATCGAGGTGATGATTTTAAAGTTGGAGCCATGAGATGATGAATGAATA 1065
QY 908 CAACATTGTTGTACAGAAAGAAAGAAACCAAAAGCATGTTTCAAGAGGAAAGC 967
DB 1066 CATAAAGCTTTTGAATATGACAAACCAACGTGAAAGCTTTGTAGCTCGTGGAGCAT 1125
QY 968 AAGGAGAGCTAGGACAGATGACTCAGCAGTGTATGATTTCCGAAAGGCAC--AAA 1024
DB 1126 ATATGCGCAAAAGGAAGTTTGAACAAAGCAATAGAAATTTTGAAGCTTGCAATTAGAAA 1185
QY 1025 GTATGCTCTGACGACAGGCGATTAGAAAGAGCTACAGCACTTGACAGCAAGAGAA 1084
DB 1186 CTGTCACTCAGAGAAATGCAAGAAATACCTCTGACAGACCTGTAGAGAGGAGAG 1245
QY 1085 AGCTTGTACCAAGAGCAAGAAATGTACAAAGAAATTTCAAGAGGAAAGATGAAAG 1144
DB 1246 ACAGTTAGAAAGAAAGAAAGTTTAAATGCTGAAGTTACTATTAAGAAAGCTTTGAC 1305
QY 1145 TGGTGCTAAGTC 1156
DB 1306 TTGGATGAGAC 1317

RESULT 14

US-09-621-976-15639/C
Sequence 15639, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jober, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15639
LENGTH: 505
TYPE: DNA
ORGANISM: *Homo sapiens*

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 18:55:30 ; Search time 829 Seconds
(without alignments)
7390.523 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270

Sequence: 1 gaaagtcgaaggtctctt.....atgaagaaggttacaatca 1270

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA:*

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16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*

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18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*

19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	533.4	42.0	1673	US-10-424-599-138705	Sequence 138705, A
2	510.2	40.9	1699	US-10-437-963-88211	Sequence 88211, A
3	486.8	38.3	1432	US-10-425-114-26760	Sequence 26760, A
4	463.8	36.5	1082	US-10-259-194A-19	Sequence 19, Appl
5	372.2	29.3	902	US-10-425-114-29666	Sequence 29666, A
6	298.8	23.0	864	US-10-259-194A-584	Sequence 584, App
7	254	20.5	376	US-09-732-627A-1173	Sequence 1173, App
8	252	19.8	469	US-10-259-194A-460	Sequence 460, App
9	210.4	16.6	1458	US-10-424-599-138708	Sequence 138708, A
10	204.4	16.1	602	US-10-437-963-88914	Sequence 88914, A
11	126.6	10.0	968	US-09-770-445-291	Sequence 291, App
12	103.6	8.2	1171	US-10-425-114-34960	Sequence 34960, A
13	103.6	8.2	2019	US-10-310-154-128	Sequence 128, App
14	102.8	8.1	1617	US-10-425-114-13768	Sequence 13768, A

15	96.6	7.6	2568	13	US-10-424-599-31694	Sequence 31694, A
16	86.4	6.8	854	13	US-10-425-114-35161	Sequence 35161, A
17	84.2	6.6	1241	16	US-10-260-228-4097	Sequence 4097, App
18	83.8	6.6	2184	17	US-10-437-963-55530	Sequence 55530, A
19	80	6.3	926	17	US-10-437-963-18428	Sequence 18428, A
20	79.6	6.3	843	13	US-10-424-599-138706	Sequence 138706, A
21	76.4	6.0	2045	13	US-10-424-599-91131	Sequence 91131, A
22	73	5.7	2835	13	US-10-424-599-17160	Sequence 17160, A
23	70	5.5	3387	13	US-10-424-599-80948	Sequence 80948, A
24	66.4	5.2	743	13	US-10-425-114-15415	Sequence 13415, A
25	65.8	5.2	728	13	US-10-425-114-23635	Sequence 23635, A
26	64.8	5.1	412	12	US-09-732-627A-3203	Sequence 3203, App
27	60.4	4.8	1727	16	US-10-260-228-488	Sequence 488, App
28	57.2	4.5	623	9	US-09-777-564-1703	Sequence 1703, App
29	57.2	4.5	623	15	US-10-015-219-1703	Sequence 1703, App
30	57.2	4.5	1812	17	US-10-283-975A-110	Sequence 110, App
31	56.8	4.5	1903	13	US-09-925-296-27	Sequence 27, Appl
32	56.8	4.5	1903	15	US-10-102-806-27	Sequence 27, Appl
33	56.8	4.5	2156	15	US-10-177-293-139	Sequence 139, App
34	56.8	4.5	2246	15	US-10-101-510-428	Sequence 428, App
35	54.4	4.3	360	12	US-09-732-627A-1572	Sequence 1572, App
36	53	4.2	2254	17	US-10-437-963-27221	Sequence 27221, App
37	52.8	4.2	2520	17	US-10-437-963-27220	Sequence 27220, A
38	52.6	4.1	2360	17	US-10-437-963-18427	Sequence 18427, A
39	51.2	4.0	641	13	US-10-424-599-80123	Sequence 80123, A
40	50.2	4.0	3387	13	US-10-424-599-80948	Sequence 80948, A
41	49.2	3.9	1002	17	US-10-437-963-9261	Sequence 9261, App
42	49	3.9	769	13	US-10-424-599-124540	Sequence 124540, A
43	48	3.8	2040	13	US-10-424-599-130000	Sequence 130000, A
44	47.2	3.7	513509	10	US-09-754-852A-4	Sequence 4, Appl1
45	46.6	3.7	2031	17	US-10-437-963-81510	Sequence 81510, A

ALIGNMENTS

RESULT 1

US-10-424-599-138705

Sequence 138705, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovacic David K

APPLICANT: Zhou Yinhua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 138705

LENGTH: 1673

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_96258C.1

US-10-424-599-138705

Query Match 42.0%; Score 533.4; DB 13; Length 1673;

Best local Similarity 68.9%; Pred. No. 7e-149;

Matches 765; Conservative 0; Mismatches 336; Indels 10; Gaps 2;

QY 144 GGAATTAATGATGATGATCTTGAGCATCAACTCAACATGACCAAGACCAAT 203

DB 186 GGAGGAAGTTCAAGAGTCTCAACCAATCATCGCTCGGTCAAGAGGAAGAAATGAAGT 245

QY 204 AGTTACTGAAGAAAGTCCGTTGTGATAGT---GCCATCTCAAGAGGTAATCTCC 259

DB 246 GATTACTGAAGAAAGTCAATTTGTAAAGGGGAACCGGACCAAGATTCAAGTGAACCC 305

QY 260 TCTTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 319

Db	306	CCCAAAAGTTGATCTGAAAGTTGAGAGTCCTTCATGAGAAAGGTGACGAACAACAAATCATTTAA	365
OY	320	GGAAAGTCACGGTTCCAAACCAATCCAAAGTACTACATGCTTTTGTCTACACAGGCAATG	379
Db	366	GGAAAGTCATGGCCGAAAGAACTTCCAAATATTTCAACTTGTCTTCCATTTACAGGCGCTG	425
OY	380	GACCAAAAACCTCGCGACCAAAATTTGAGAGTATCATGAGATAGACGACCACTATTTGAATTT	439
Db	426	GCGTGAAGATACACACACAAAGTTTGAAGACATAGGACGAGGACAAAGCCCAATTTGAAT	485
OY	440	GGTTCTTGAAAAAGAAAAAGAACTAGCCGGTTTACCAATCGGTGTTGCTAGCATGAA	499
Db	486	GGTCTTAGGAAAAAGAAAAAGAAATGACTGGGTGTGGCAATTTGGTGTGGCAAGATGAA	545
OY	500	GTTCTGTGAACGTGGCGCTTTGTGCATGTTGGCTGGGAATTAGCTTAATGGAAAAAGAGAAA	559
Db	546	AGCTGGGAGCGGGGGTGTGGTCCGTGTGGGCTGGGAATTAGAGTATGAGAGGAAGGAAG	605
OY	560	CTTTTCTTTTCCCAATGTTCCACCATGAGGACACTGTTATATGAGTGGTGAAGTATTAG	619
Db	606	CTTCTCTTTTCCAAATGTTTCCACCACAGCGCAATTTAGTTTATGAAAGTTGAGCTCATTTGG	665
OY	620	GTTTGATGAAACAAAGAGGAGAAAAAGCTCGCAGTATATGACTGTAGAGAAAGATTTGG	679
Db	666	CTTTGATGAAACCAAGAAAGGCAAAAGCTCGCAGTATATGACTGTGAAAGAAAGATTTGG	725
OY	680	TGCAGCACACAGAAAGAAAAATGAGATGGGAATTTCTTTTAAAGAGAGAAACTGAGAGA	739
Db	726	TGCAGCACACCGGAGAAAAAGATGGAATGGAATGCTTTGTATCAGGAAGAAAAACTAGAGGA	785
OY	740	AGCCATGCAACAGTATGAAATGAGCCATATGACATACATGAGGAGCACTTTATGTTTCACTT	799
Db	786	GGCTATGCAACAGTATGAAATGAGCCATATGACATATATGGGAAGTGACTTCATGTTTCCAGGG	845
OY	800	GTATGGGAAGTACCAAGATATGCGCTTTAGCAGTTAAAAAACCATGCCATCTTAACATAGC	859
Db	846	CTGCGAAAGACGAACAGAGGGGGCTCTGGCAGTAAAGATCATGCCATCTTTAACATGGC	905
OY	860	AGCTTGCTCTCATCAAATCTAAAAACGATACGATGAGACCAATTTGCTACTCTGCACATTTGTCTT	919
Db	906	AGCCTGTTGATTAAAGCTGAAACCGCTGAGAAAGACCATAGACATCATCACACATTTGACT	965
OY	920	GACAGAAAGAGAAAAAACCCAAAAAGCACTGTTGCAAGAGGAGAAAGCAAAAGCGAGACT	979
Db	966	GGGTGAGGATGAGAACCAATGTGAGGCACTTATTTTAGGCGAGGTAAAGCTTAGACAGCACT	1025
OY	980	AGGACAGATGACTTCAGCAGCAGTGAATTTCCGAAAGGCACAAAAGTATGCTCTTGACGA	1039
Db	1026	TGGGCAAAACGATACTGCGCAGGGAAGATTTCTTAAAGGCAAGTAAATATGCCCCCTCAAGA	1085
OY	1040	CAAGCGGATTAGAAAGAGGCTTACGAGCACTTGACGAGGAGAAAGAAAGCCTTGTCACAAA	1099
Db	1086	CAAGGCAATTCCTAAAGATTGAGATGTTGCTTGCTGAAATATGACAAAGGCTGTTTACAAA	1145
OY	1100	GCAGAAAGAAATGTACAAGGAATTTTCAAAGGGAAGAAATGAAGGTGTGCTTAAGTCAA	1159
Db	1146	GCAAGAAAGAAATATATTAAGGAATTTTGGACCAAGGCTCAACCAAGTTCTTAAGCCAAAG	1205
OY	1160	GAGCCTTTTGTGTGATATGTTATGSCAAATGTTTGTTCCTTTTCTCCCGTATCTT	1219
Db	1206	AA-----ATTGGCTCATACTTATTTTGGCAAGTGTGCTTCAAGTATCTATGCGCTTGT	1259
OY	1220	TCGACGCCACAGATTTAAAGCAAGTAAATGT	1250
Db	1260	CACGCTCTTCAAGGCTCAAAGGCATAAATCT	1290

```

1  APPLICANT: Kovalic, David K.
2  APPLICANT: Zhou, Yihua
3  APPLICANT: Cao, Yongwei
4  APPLICANT: Wu, Wei
5  APPLICANT: Boukharov, Andrey A.
6  APPLICANT: Barbazuk, Brad
7  APPLICANT: Li, Ping
8  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
9  TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
10 FILE REFERENCE: 38-21(53221)B
11 CURRENT APPLICATION NUMBER: US/10/437,963
12 CURRENT FILING DATE: 2003-05-14
13 NUMBER OF SEQ ID NOS: 204966
14 SEQ ID NO 82511
15 LENGTH: 1699
16 TYPE: DNA
17 ORGANISM: Oryza sativa
18 FEATURE:
19 OTHER INFORMATION: Clone ID: PAT_MRT4530_81934C.1
20 US-10-437-963-82511

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Query Match	40.2%	Score 510.2	DB 17	Length 1699
Best Local Similarity	72.3%	Pred. No. 6,66-142		
Matches 676	Conservative 0	Mismatches 258	Indels 1	Gaps 1
QY	193	GAGAGGAAATAGTACTGAGAGAAAGTCCGCTTGATGATGTC-GCCATCTCAAGAGGT	251	
Db	1410	GATTAATGAGATTAAGTCTAGAGAGACCTTTTGTGATTAAGAACTCCGCAAGATGGC	135	
QY	252	AATGTTCTCTTAAAGTTGATGTGAAGCTGAAGTCTTGATGAGAAAGTCAGTAAGCAG	311	
Db	1350	TCTGTCCCACTGTGGTTTCTCTAATATGAGAGGTCTTCAATGACAAAGTTAAAAACAA	129	
QY	312	ATTATTAAGGAAGGTGACGGTTCGAAACATCCGAAGTACTCAATGCTTTTGACTAC	371	
Db	1290	GTCATTAAGAAAGGCCATGGAAGAACCATCAAAAGTTGCGAGTGTCTTTTGCACTAT	123	
QY	372	AGGCACTGAGACCAAAAACTCGACGACAAATTTGAGATACATGCGATGAGACCAACT	431	
Db	1230	AGAGCTTTGGGTTCAAGCGTCTCTGATTAATTCAGAGATACCTTGCAAGAACAGCATCC	117	
QY	432	ATTGAATTGGTCTTTGGAAGAGAAAAAGAACTAGCCGGTTTATGCCATCGGTGTCT	491	
Db	1170	ATTGAAGTGTATTTGGAAGAAAGAGAAAAACAATGTCTGGTTTATGAGCATTTGGTGTGGT	111	
QY	492	AGCATAAAGTCGTGGGAAGTCGCTGTGATGATGTGGCTGGGAATTAGCTTATGGGAAA	551	
Db	1110	AACATGAGAAATGGGGAGCGTCACTGTGATGTGGCTGGGAGTAAAGCTATGGGAAA	105	
QY	552	GAGAGAACTTTTCTTTTCCCAATGTTCCACTATATGCGAGACTTGTTATATGAGGTGAA	611	
Db	1050	GAAAGGAGCTTTTCAATCCCAATATCCCTCAATGGAGATCTTTTATATGAAGTTGAA	991	
QY	612	GTTATTGGGTTGATGAAAAAAGAGAGGAAAAAGCTGCACTGATATGACTGTATAGAGAA	671	
Db	990	CTTATTGGGTTTGATGATGTCAAAAGAGGGGAAAGCCGAGTGCATGACAGATGAGGAA	931	
QY	672	AGGATGTGGTGCAGCGACAGAGAAAGAAATATGATGGAAATTCCTTTTATAGAGAGGAAA	731	
Db	930	AGGATTTGAAGCAGCGGACAGAGGAAGATTGAGGCAATGATATTTCAAGAGAAAGAA	871	
QY	732	CTGAGAGAAAGCATGCAACAGATGAAATGGCCATAGCATATCATGGGGAGCGATTTTATG	791	
Db	870	TTTGAAGAGGCGATGAGCAATATGAATATGGCATGTATACATGGGAGATGACTTCATG	811	
QY	792	TTTCACTGTATGGGAAGTACCAGATATGCTTTAGCATTTAAAAACCATGCCATCTT	851	
Db	810	TTTCAATTTGTTGGGAAATACAGAGATATGGCTTTGGCTGTGAAAAATTCATGTCACTTC	751	
QY	852	AACATGACAGCTTGCTCATCAAATTAAGATACATTAAGCAATTTGCTCACTGAC	911	
Db	750	AACATGGCCGATGCTTAATCAAACTGAAGAGATTTCATGAAGCTTATCGACAGGTAGT	691	

Query Match	38.3%	Score 486.8;	DB 13;	Length 1432;
Beat Local Similarity	71.7%	Pred. No. 6.3e-135;		
Matches 638;	Conservative 0;	Mismatches 252;	Indels 0;	Gaps 0;
<p>Query 237 CCATCTCAAGAGGGTAAATGTCCTCCTCTTAAGTTGATGAGAGCTGAGGCTTGATGATGAG 296</p> <p>Db 233 CTTCCCAAGAGATGGCAGCCGCCCACTGGTGTCTCTGACATGAGAGGCCCTTACAGAC 292</p> <p>QY 297 AAGTCAGTAAACAGATTATTAAGAAGGTCAAGGTTCCAAACCATCAAGTACTTACA 356</p> <p>Db 293 AAGGTTAAGAACCAATATATCAAGAAGGCCATGACAGAAACCGCTGAAGTTCCGAGAG 352</p> <p>QY 357 TGCCTTTGTCACTACAGGGCATGACCAAAAACCTGCAGACCAATTTGATGATACATGG 416</p> <p>Db 353 TGCTTTGTGCTATGAGCATGAGGTTCAAGATCATCCATTAATTTGAGATACCTGG 412</p> <p>QY 417 CATGAGCAGCAACCTATTGAAATTTGGTCTTGGAAAAAGAAAAAACAACCTAGCCGTTTA 476</p> <p>Db 413 CAAGAGCAACATCCCAATTTAAGTACCTTGGAAAAAGAAAAAACAATGCTGTGTTTA 472</p> <p>QY 477 GCCATCGGTGTGCTAGCATGAAGTCTGGTGAACGTGCGCTTGTGATGATGCTGGGAA 536</p> <p>Db 473 GGCAATCGGTGTGCTAGCATGAAGTCTGGTGAACGTGCGCTTGTGATGATGCTGGGAA 532</p> <p>QY 537 TTAGCTTATGGAGAAAGAAAGAACTTTTCTTTTCCCAATGTTCCACTTATGCGACCTTG 596</p> <p>Db 533 CTAGCGCTATGAGAAAGAAAGAAAGTCTTTTCTTTTCCCAATGTTCCACTTATGCGACCTTG 592</p> <p>QY 597 TTATATGAGGTGGAAGTATTGCGTTTGTATGAAACAAGAAGGAGAAAGTCTGCAATGAT 656</p> <p>Db 593 GTTATGAGGTGGAAGTATTGCGTTTGTATGAAACAAGAAGGAGAAAGTCTGCAATGATGAT 652</p>				

QY	ATGACTGAAGGAAAAGATTGGTCAGACAGACGAAGAAAATGATGGCAATTCCTT	716
Db	653 ATGACAGTTGAAGAGAGGAATTGGCTGCTGCACACAGAGAAAAGATTGAGGCAATGCATAT	712
QY	717 TTTAAGAGAGAAACTGAGAGAAAGCCATGCAACGATATGAAATGGCCATATGATCATG	776
Db	713 TTCAAGAAAAGAAAGCTTTGAGAGAGGCCATGACGACAAATATGAAAATGGCATTTGCATTAATG	772
QY	777 GGGACACATTTATGTTTCAGCTGTATGGGAAATGACAGATATGGCTTTATGACAGTTAAA	836
Db	773 GGAATGATTTTCATGTTTCATTTATTTGAAAGTACAGAGCATGGCCTTGGCTGTGAAA	832
QY	837 AACCCATGCCATCTTAAACATAGCAGCTTGCCTCATCAAACTTAAAACGATACGATGAAGCA	896
Db	833 AATCATGTCATCTCAATATATGGCTGCAATGCCCTGATCAAACTTAAAGATTTGATGAAGCT	892
QY	897 ATTGGTCACTGCAACATTTGTGTTGACACAGAGAGAGAAAAACCAAAAGCATGTTTCA	956
Db	893 ATTCCGACGTGTACCATTTGTTTACACAGAAATGAAATGATATGTCAAAGCCCTGTTACGG	952
QY	957 AGAGGAAAGCAAAAGGACAGACTGACAGATGACCTGACGACGTCGATGATTTCCGAAAG	1016
Db	953 CGAGGAAAAGCTTAATCTGAATCTTGACACAGACAGAAATCAGCGAGGAAAGATTTCTCAAA	1012
QY	1017 GCACAAAAGTATGCTCTCTGACGACAAAGCGATTTGAAAGAGACTAGACGACCTTGCAGAG	1076
Db	1013 GCGAAGAAAGTACTCCCGAAGAAACAAGAGATCATTTGGGAGGCTCCGTTTGCTCGCGGAA	1072
QY	1077 CAAGAAGAAAGCTTGAACCAAAACGACAAAGAAATGTATCAAAAGGAATATT	1126
Db	1073 CAAGAAGAGCACTATATACAGAAACGAAAGAGGCTTATCAAAAGGTTCTTT	1122

```

RESULT 4
US-10-259-194A-19
; Sequence 19, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghassemlan, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazedbrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyuki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 19
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-194A-19

Query Match      36.5%; Score 463.8; DB 16; Length 1082;
Best Local Similarity 72.0%; Pred. No. 4.3e-128;
Matches 675; Conservative 0; Mismatches 252; Indels 10; Gaps 5;

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OY	199	AAATAGTACTGAAAGGAAGCGGTTGATAGTGGTGGCATCTCAAGAGGTAATGTT	257
Db	34	GAGATACAGTGGAAAGAACTTCTTGTTGATACAGGCTCTCAAGATGGACGTGCT	93
OY	258	CCTCTTAAGTTGATAGTGAAGCTGAGGCTCTTGATGAGAAAGTCAGTAAGCAATTATA	317
Db	94	CAACTGTGTGTTA CCTGTATATGGAATCCTTATATGATTAAGTCAAAAACAAAGTCATC	153
OY	318	AAGGAAGTCAAGGTTCCAAACCATCCAATCTACATGCTTTTGTCACTAAGGGCA	377
Db	154	AAGGAAGCCATGGCGAAGAAACCTCCAAAGTTTGGCAGATCTTTT--GCATTAATGAGCA	211
OY	378	TGSAACCAAAA CTGCAAGCAAAAATTGAGATTCATAGGCAATGAGCAAGCAATATGAA	437
Db	212	TGGGTTCAAGGTTCTTGGCAACAATTCAGAGATACCTGGCAAGAACAGCATTCAAATTGAA	271
OY	438	TTGGTCTTGGAAAA--GAGAAAAAAGACTAGCCGTTTACCATCGGTGTTGCTAGCAT	496
Db	272	CTAGTACTTGGAAAAAGAAAAAGAAATGACTGGTTTAAAGCATTGGTGTCAATACAT	331
OY	497	GAAGTCTGTGAACGTGCGCTTGTGCATGTTGGCTGGGAATTTAGCTTAATGGAAAAAGG	556
Db	332	GAGAAGTGGGAGCGTGCATTGTTATACATGTTAACTGGGAGCTTGGCTATGGGAAAGAG	391
OY	557	AAACTTTTCTTTCCCATATGTTCCACTATAGCAGACTTGTATATAGGTGGAAATAT	616
Db	392	AAGCTTTTCATTTCCCAAAATGTCCTCCAAATGCGACACTGTATATGAAGTTGAACCTAT	451
OY	617	TGGGTTTGATGA--AACAAGAGAGGAAAGCTCGCAGTATGATGACTGTAGAAAAAGA	675
Db	452	TGGGTTTGATGATGTCAAAAGAGGGGAAAGCCGAAGTGAATGACAGTGGAAABAAAGA	511
OY	676	TTGGTGCAAGCAAGAAATAATGATGGAAATTCCTTTTTPAAGGAGAGAACTGG	735
Db	512	TTGGAAGCAGCAGACAGAGAAAGATTTGAAGCCAATGATATTTTCAAGAAAAAGAACTGG	571
OY	736	AGGAAGCATGCACAGATGAATAATGGCATATAGCATATAGGGGAGCATTTTATGTTTC	795
Db	572	AGGAGGCTATCAGCAATATATGAATAATGGCAATTTGACATATAGGGGATATTTTCAATGTTTC	631
OY	796	AGCTGTATGGGAAGTACCAAGATATGCTTTAGCAGTTAAAAACCATATGCATCTTAA	855
Db	632	AATGTGTTGGGAAGTACAGACATATGCTTTAGCTGTGAATAAAATCCCTGCATCTCAACA	691
OY	856	TAGCAGCTTGCCTCATCAAACTTAAACGATACGATGAAGCAATTGTCACATGCAACA--	912
Db	692	TGGCCGACATGCTGATCAAACTGAAGAGATTTGATGAAGCTATATGCCCCAGTATACAT	751
OY	913	--TTGTGTGACAGAAAGAAAAAACCCAAAAGCACTGTTTCAGAAAGGAAAAAGCAAA	970
Db	752	GTATGTGTTGTGCAAGAGATGA AAAACMAAGTGAAGCGTTGTTTCAGACAGAGAAAAAGCTAG	811
OY	971	GAGCAGAGCTAGACAAGATGGA CTGACAGCTGTATGATTTCCGAAAGGCACAAAAGTATGC	1030
Db	812	AGCTGAATCTTGTCAAACAGATCAGCAAGGAGGACCTTCTGAAAGGCCAAAGAAATATTC	871
OY	1031	TCCTGACAGACAAGCGATTAGAAAGAGACTTACAGCACTTTCAGACAGCAAGAAAGCCTT	1090
Db	872	TCCAGAAAGACAAGAGGATCCAGCGGAGACTTCGGTCCGTCGCGGAGCAGATTAAGCTCT	931
OY	1091	GTACCAAAAGCAAAAAGAAATGTACAAAGAAATATTC	1127
Db	932	GTACCAAGAAACAAAAGAGCTATTAACAAAGCTGTGTTCT	968

RESULT 5
US-10-425-114-29666
; Sequence 29666, Application US/10425114 ;
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jigdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.

```

: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21,533(B)
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 29666
: LENGTH: 902
: TYPE: DNA
: ORGANISM: Glycine max
: FEATURE:
: OTHER INFORMATION: Clone ID: UC-GMFLMINSOY112G04_FLI
US-10-425-114-29666

```

Query Match	29.3%;	Score 372.2;	DB 13;	Length 902;
Best Local Similarity	-72.9%;	Pred. No. 1.2e-100;		
Matches 495; Conservative	0;	Mismatches 178;	Indels 6;	Gaps 1;

QY	531	GGGAATTAGCTTATGGGAAAGAAAGAAACCTTTCTTTCCATGTCTCCACTATGGCA	590
Db	1	TGGAAATTGAGATATGAGAGGAAAGAAAGCTTCTCTTTCCAAATGTTCCACCAGGCA	60
QY	591	GACTTGTATTATVAGAGTGGAGATTATGCGTTTGATGAAACAAAGAGGGGAAAAGCTGCG	650
Db	61	GATTAGATTATVGAAGTTGAGCTCATTTGGCTTTGATGAAACCAAGAGGCAAAAGCTGCG	120
QY	651	AGTATATATGATGTAGAGGAAAGGATTTGGTSCACAGACAAAGGAAAAATGGATGGGAAT	710
Db	121	AGTATATATGACTGTGGAGAAAGATTTGGTSCACAGACCCGGAAGAAATGGATGGGAAT	180
QY	711	TCTCTTTTAAAGAGAGAAACTGAGAGAACCATGCAACGATGAAATGGCCATAGCA	770
Db	181	GCTTTGTATCAGAGAAAGAAAACCTAGAGAGGCTATGCAACGATGAAATGGCCATAGCA	240
QY	771	TACATGGGGGACGATTTTATGTTTCACTGTATAGGAAATGACAGAAATAGGCTTTAGCA	830
Db	241	TATATGGAGATGACTTCATGTTTCAAGTTGTTTGGAAATATAGAGATATGGCTTGACT	300
QY	831	GTTTAAAAAACCCATSCCATCTTAAACATAGCAGCTTGCCCTCATCAAACTAAAACGATACGAT	890
Db	301	GTAAGAATCCATGCCATCTTAAACATGGCAGCCGTGTTGATTAAAGCTGAAACGGTACGAA	360
QY	891	GAGCAATTGGTCACTGCAACATTGTGTGACAGAGAAAGAAAACCCAAAAGCACTG	950
Db	361	GAACTATAGACACATGCAACACTGTACTGGGTGAGATGAGAAACAATGTAAAGCCGTTA	420
QY	951	TTGAGAGAGGGGAAGCAAGGACAGAGCTAGACAGATGACCTCAGCAGCTGATGATTTG	1010
Db	421	TTTGGCGAGGTAAAGGCTTAGGCAACACTTTGGCAACAGATGCTGCCAGGGAAAGATTTT	480
QY	1011	CGAAAGCACAAAAGTATGTCTCTGACGACAAGGCGATTAGAGAGAGCTACGAGCACTT	1070
Db	481	CTAAGGCGAACTTAATATATGCCCCCTCAAGACAAACCAATTGCTAAAGATTAGAGTTGCTT	540
QY	1071	GCAAGACAAGGAAGACCTGTACCAAAAGGAGAAAGAAATGTCAAAAGAAATTTCAAA	1130
Db	541	GCTGAACATGCAAGGCTGTTTACCAAAAGGAGAAAGATATTAAGGAATTTTGGCA	600
QY	1131	GGGAAAGATGAAGGTGTGCTTAAGTCAAAAGACCTTTTGTGTTGATATAGTTATGGCAA	1190
Db	601	CCAAAGGCGCTCAACCAAGTTCTTAAGCCAAAGAAAC-----TGGCTCATCTTATTTGGCAG	654
QY	1191	TGAGTTTGTTCCTTTTCT	1209
Db	655	TGAGTTTGTTCAGATTTCT	673

RESULT 6
US-10-259-194A-584
; Sequence 584, Application US/10259194A

```
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghaseemian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 70029-NP
; CURRENT APPLICATION NUMBER: US/10/259,194A
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,743
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 662
; SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 584
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Trifolium aestivum
US-10-259-194A-584
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Query Match      23.5%; Score 298.8; DB 16; Length 864;
Best Local Similarity 73.4%; Pred. No. 1.3e-78;
Matches 395; Conservative 0; Mismatches 142; Indels 1; Gaps 1;

QY 589 CAGACTTGTATATGAGGTGAGAGTTATGGGTTTGTGTAACAAAGAGAGGAAAGCTC 648
DB 1 CAGACCTTATATATGAGTTGAACTCAAT-GGTTTGATGTGCTAAAGAGGAAAGCTC 59
QY 649 GCAGTATATGACTGTATGAGAAAGATTGTGTCAGACAGACAGAAAGAAATGATGCGA 708
DB 60 GTATGTACATGACGATGAGAGAGAGATTGAAACAGCGGATAGAGAGAACTTGAGGCGA 119
QY 709 ATTCTCTTTTAAAGAGAGAACTGAGAGAACCATGCAACATATGAAATGCGCATAG 768
DB 120 ACGATTACTTTAAAGAGAAATTTGAGAGGCTATGACAGCAATATGAGATGCGTGTG 179
QY 769 CATACATGGGGAGCATTTTATATGTTTCACTGTATGGAAGTACAGAGATATGGCTTTAG 828
DB 180 CGTATATGGAGATGATTTATGTTTCACTGTTTGGGAAGTACAGAGATATGCTTTGG 239
QY 829 CAGTTAAAAACCATGCGCATCTTAACTATAGCAGCTTCCATCAAACTAAAAGATACG 888
DB 240 CTGTGAAAAACCCGTGCGATCTCAACATGCGCTGCTGCTGATCAAAAGAGATTTG 299
QY 889 ATGAGCAATTTGCTCACTGCAACATTTGTTGA CAGAAAGAGAAAAACCAAAAGCAC 948
DB 300 ACGAACTATCGACAGTGTAGCATTTGTCTGT CAGAGAGCAAAACCAAGTAAAGCGC 359
QY 949 TGTTCAGAAAGGAGAAAGCAAGCAAGCTATAGACATGAGTCAAGCAGTATGATT 1008
DB 360 TGTTCAGACGTGAGAAAGCTGAGCGAGCTCGGCCAGACAGATCAAGCAGAGAGACT 419
QY 1009 TCCGAAGGCAAAAGTATGCTCTGACGACAGAGCGATTAGAAAGAGCTACGAGAC 1068
DB 420 TCTTGAAGGCAAGAAACATCCCGCGAAGACAGAGATCAAGCGGAGCTTCGGTGC 479
QY 1069 TTGCAAGCAAGAGAAAGCTTGTATCCAAAGAGAGAAAGATGTATCAAAAGATATT 1126
DB 480 TGGCGAAACAAAGATAAAGCATGTACAGAGAGAGAGGAGTATACAAAGTCTGTT 537
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```
RESULT 7
US-09-732-627A-1173
; Sequence 1173, Application US/09732627A
; Publication No. US2004012338A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(51770)B
; CURRENT APPLICATION NUMBER: US/09/732,627A
; CURRENT FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 4930
; SEQ ID NO 1173
; LENGTH: 376
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(376)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3493-057-Pl-M1-C7
US-09-732-627A-1173
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Query Match      20.0%; Score 254; DB 12; Length 376;
Best Local Similarity 80.4%; Pred. No. 2.2e-65;
Matches 296; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
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QY 462 GAACCTAGCCGGTTTACCATCGGTGTTGCTAGCATGAAGCTGTGTAACGTGCGCTGTG 521
DB 8 GAATGACTTTTGTGGTATGCGTGTGTCAGATGAAATCANGAAGCGTGCATTGTTA 67
QY 522 CAGTTGGCTGGGAATTTACTCTTATGAGGAAGAAAGAACTTTCTTCCATGTTCCA 581
DB 68 CAGTGGCTGGGAATTTAGATATGAGGAAGAAAGCTTTCTTCCAAAGCTTCCA 127
QY 582 CCTATGCGACACTTGTATATGAGGTGAGTGAAGTATTTGGTTGATGAAACAAAGAGAGA 641
DB 128 CCAATGCGACATATATATATGAGGTGAGCTTATTTGATTTGACAAACCAAGAGAGA 187
QY 642 AAAGCTCGCAGTATATGACTGTAGAGAAAGATTTGTGACAGACAGACAGAAAGAAATG 701
DB 188 AAGGCTCGTGTGACATGACTGTAGAGAAAGATTTGTGACGCGATGAAAGAAATG 247
QY 702 GATGGAATTTCTTTTAAAGAGAGAACTGAGAGAACCATGCAACATATGAAATG 761
DB 248 GACGGGAATTTCTTTTAAAGAGAGATTAAGCTTAGAGAGCGCATGCAACATATGAAATG 307
QY 762 GCCATGCAATACATGGGGAGCATTTTATGTTTCACTGTATGGAAGTATGCCAGATTAG 821
DB 308 GCCATAGCGTACATGGGTATGATCTTTATGTTTCACTGTTATTTGGAGAGATGAGACATG 367
QY 822 GCTTTAGC 829
DB 368 GCTTTAGC 375
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RESULT 8
US-10-259-194A-460/c
; Sequence 460, Application US/10259194A
; Publication No. US20040010815A1
; GENERAL INFORMATION:
; APPLICANT: Lange, Markus B.
; APPLICANT: Ghaseemian, Majid
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
```

```

? TITLE OR INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
? FILE REFERENCE: 70029-NP
? CURRENT APPLICATION NUMBER: US/10/259,194A
? CURRENT FILING DATE: 2003-01-07
? PRIOR APPLICATION NUMBER: US 60/325,277
? PRIOR FILING DATE: 2001-09-26
? PRIOR APPLICATION NUMBER: US 60/370,743
? PRIOR FILING DATE: 2002-04-04
? PRIOR APPLICATION NUMBER: US 60/370,620
? PRIOR FILING DATE: 2002-04-04
? NUMBER OF SEQ ID NOS: 662
? SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
? SEQ ID NO 460
? LENGTH: 469
? TYPE: DNA
? ORGANISM: Musa acuminata
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (251)..(251)
? OTHER INFORMATION: n = any nucleotide
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (352)..(352)
? OTHER INFORMATION: n = any nucleotide
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (366)..(366)
? OTHER INFORMATION: n = any nucleotide
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (383)..(383)
? OTHER INFORMATION: n = any nucleotide
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (437)..(437)
? OTHER INFORMATION: n = any nucleotide
? IS-10-259-194A-460

```

```
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barabuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 88914
LENGTH: 602
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_8771C.1
US-10-437-963-88914

Query Match      16.1%; Score 204.4; DB 17; Length 602;
Best Local Similarity 65.6%; Pred. No. 2.4e-50;
Matches 298; Conservative 0; Mismatches 156; Indels 0; Gaps 0;

QY 199 GAAATAGTTACTGAGAGAGAGTGGCTTGTGATAGTGGCCATCTCAAGAGGTAATGTC 258
DB 149 GAGATACGAGGAGATTAATCTCTGTGTGCACTGAACCTCTTGATGGATGCTGCTC 208
QY 259 CTCTTAAGTTGATAGTGAAGCTGAGGTCTTGTGATGAGAAATGCAATGATTAATTA 318
DB 209 CACCTGTGCTTACCTGTGATATGAGAGCCCTTAATATGTAAGCCAGAAACCAAGGCAATCA 268
QY 319 AGGAAGTGCAGGTTCCAAACATCCAAAGTACTCTACATGCTTTTGTGCACTACAGGCGAT 378
DB 269 AGAATATCCATGCGAAGAAACCTCAAGTTTGACACATCTTTGTTCACTATACAAAT 328
QY 379 GGAACAAAACCTGCGACACAAATTTGAGATACATGAGTGAAGCAACCTATTAAT 438
DB 329 GGGTTCAGGTTCTTGCAAAATTTGAGATACATGAGTGAAGCAACCTATTAAT 388
QY 439 TGGTCTTGAGAAAGAGAAAGAAAGAAATAGACCGTTTACCGTGTGCTAGCATGA 498
DB 389 TAGTACTTGGAAACAGAAAGAAAGAAAGTGAATGCTGTGCTGAGCCACTAATACATGA 448
QY 499 AGTCTGTGAACGCTGCTGTGATGATGCTGGGAATTAAGCTTATGGAAGAAAGAA 558
DB 449 AAGAGAGGAGCGCTGCTTGTACATGATGATGCGAGCTTGGCTATGTAACAGAA 508
QY 559 ACTTTTCTTTTCCCAATGTTCACTATGCGAGACTTGTATATGAGTGAAGTTATG 618
DB 509 GCTTTTATCCCAAAATGTTCTTCAATGCGAGCCCTGTATATGAAGTGAATCAATG 568
QY 619 GGTTCATGAACCAAGAGAGAGAAAGCTGCGAG 652
DB 569 GGCCTGATGATGTCAACAGAGAAAGCCCGAAG 602

RESULT 11
US-09-770-445-291
Sequence 291, Application US/09770445
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
```

```
APPLICANT: Page, Amy
APPLICANT: Matthew, Abraham V.
APPLICANT: Bedford, Brooke L.
APPLICANT: Moessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Kicker, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 291
LENGTH: 968
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-770-445-291

Query Match      10.0%; Score 126.6; DB 9; Length 968;
Best Local Similarity 77.7%; Pred. No. 7.6e-27;
Matches 178; Conservative 0; Mismatches 49; Indels 2; Gaps 2;
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QY 436 AATGTTCTTGGAAAGAGAAAGAAAGAAAGTACGCGGTTAGCCATCGGTTGCTAGCA 495
DB 68 AATGCTCTATGAAAGAGATACAGTATAGCGCGGTTAGCTATGTTGTTCCAGCA 127
QY 496 TGAAGTCTGTGAACGCTGCTGTGATGTTGCTGGAA--TTAGCTATGGAGAA 554
DB 128 TCAAGTCTGTGAACGCTGCTGTGATGTTGCTGGAAATTTAGCATATAGAGAGAT 187
QY 555 GGAACCTTTTC--TTTCCCAATGTTCCACCTATGCGAGACTTGTATATGAGTGAAGT 613
DB 188 GGAACCTTTCTTTTCCCAATGTTCCATCTATGCGGAGATTTGATGAGACGCTGAGT 247
QY 614 TATGTTGTTGATGAAACAAAGAGAGAAAGTCCCATGATATGACT 662
DB 248 TGTGATTTGATGAAACAAAGAGAGACGTTTTCCTTAAGATCAT 296

RESULT 12
US-10-425-114-34960
Sequence 34960, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 34960
LENGTH: 1171
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-2MFLMO17365D08_F11
US-10-425-114-34960
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Query Match      8.2%; Score 103.6; DB 13; Length 1171;
Best Local Similarity 48.8%; Pred. No. 6,9e-20;
Matches 410; Conservative 0; Mismatches 409; Indels 21; Gaps 4;

QY      291 GATGAGAAAGTCAGTAAAGCAATTAAGAGAAAGTCAAGGTTCCAAACCATCCAAATAC 350
      44 GATAGAGAAATCCCTTAAGAGGTTCTCAAGAGGAGAAAGTTATGAGCGTCCCAAG 103
QY      351 TCTACATGCTTTTGCTACAGAGGCAATGACCAAAAACCTCGACGCAAAATTGAGAT 410
      104 GGTGCTGTGTGTAAGTCAAAATTAATCGGAAAGCTTCAGATGCGCGGTGTACAAAG 163
QY      411 ACATGCGATGAGCAAGCAACCTATTGAATTGGTTCTTGAAAGAGAAAAAGAACTAGACC 470
      164 AAGGGGATGACGAAAGAGCCATTTAATTCAAGCCGATGAAGG---GAAGTTATTGCC 220
QY      471 GGTTAAGCCATCGGTGTGCTAGCATGAAGTCTGCTGACAGTGGCGCTTGTCATGTTGGC 530
      221 GGTCTTGATCGTGTGTTGAAATGATGAAAGGCGAGGTTGCTTGTGCACAAATTCCT 280
QY      531 TGGGAATTAGCTTAAGG---AAAGAAAGAAACCTTTCTTTCCCAATGTTCCACCTAG 587
      281 CTTGAATATGCAATTTGTTCACTGACGCAAGAGAGATCTTGCTGTTTCCACTTAC 340
QY      588 GCAGACTTGTATATAGAGTGAAGTGAATGAGTTGGTTGATGAAACAAAGAGGAGAAAGCT 647
      341 AGCAGATATATATGAAAGTTGAGCTTATTCAATTTTGAAAGCAAGAGTGTG----- 395
QY      648 CGCAGTATATGACTGTAAGAGAAAGATTTGTCAGACAGACAGAGAAAAATGATGGG 707
      396 ---GGGACTTGAACAATGAAGAGAAATGAGGCTGCTGTGAAGAAAGAGAGGG 451
QY      708 AATTCCTTTTAAAGAGAGAAACGTGAGAGAGCCATGCAACATGATGAATGAGCAT 767
      452 AATGCAATTGTTCAATGCGCAAAATATCTAGAGCTTCCAGGATATGAGAGGCTGCC 511
QY      768 GCATACATGAGGAGCAATTTATGTTTCACTGATGAGAGTAAACAGATATGCTTTA 827
      512 AAGTACATTAAGTATGACACCTGCTTCAAGTGAAGTGAAGAAAGCAATCCAG----- 565
QY      828 GCACTTAAAAACCATGCTTCTTAATATGAGAGCTTGCCTCATCAAACTAAAAAGATAC 887
      566 CAACTGAAGATCAGCTGCAACTTAACAATGCTGCCGCAACGAAAGTTGAAGATTAAC 625
QY      888 GATGAAGCAATGTTGCTCACTGCAACATGTTGTCAGAGAAAGAGAAACCCAAAAGCA 947
      626 AAGGAGCTCGAAGCTTTTGACACCAAGTTCTGGAATGACAGCCAAAATGTCAGAGCT 685
QY      948 CTGTTCAAGAGAGGAGAAAGCAAGGCAAGCTTAGAGACATGATGACGACGTGATGAT 1007
      686 CTCTACAGAGAGGAGGCTTACATTCATCACTTGCTGACTAGAGCTAGAGAGGCGGAT 745
QY      1008 TTCCGAAAGGCAAAAAGTATGCTCTTGAAGCAAGGCGCATTAAGAGAGCTTAGAGCA 1067
      746 ATCAAAAAGGCACTGGAATCGATCTGACACAGAGGATGTCAAGTTGAATTAAGATC 805
QY      1068 CTTGACAGAGAGAGAAAGCTTGTACCAAAAGCAAGAAAGAAATGTCAAAGAAATTTTC 1127
      806 CTGAAGAGAAAGATCAAGAGATACACAAAGAGAGCCCAAAATTTCTACAGCAATGTTCC 865

```

```

; APPLICANT: Banu, G.
; APPLICANT: Bell, Erin
; APPLICANT: Boddupalli, Raghava
; APPLICANT: Deikman, Jill
; APPLICANT: Deng, Kolian
; APPLICANT: Dong, Jinhua
; APPLICANT: Duff, Stephen M.
; APPLICANT: Galligan, Meghan M.
; APPLICANT: Hinchey, Brenda S.
; APPLICANT: Huang, Shihshieh
; APPLICANT: Johnson, G. Richard
; APPLICANT: Jung, Vincent
; APPLICANT: Kretzmer, Keith A.
; APPLICANT: Laccetti, Lucille B.
; APPLICANT: Lai, Chao-Qiang
; APPLICANT: Lee, Gary
; APPLICANT: Lin, Jie-Yi
; APPLICANT: Liu, Jindong
; APPLICANT: Lu, Bin
; APPLICANT: Luehly, Michael M.
; APPLICANT: Lund, Adrian
; APPLICANT: Madson, Linda L.
; APPLICANT: Mallory, Kathleen A.
; APPLICANT: McKiel, Christine L.
; APPLICANT: Miller, Philip W.
; APPLICANT: Padavathi, ManchiKanti
; APPLICANT: Parnell, Laurence D.
; APPLICANT: Start, William G.
; APPLICANT: Temmesen, Dan
; APPLICANT: Vidya, K.R.
; APPLICANT: Wang, Haiyun
; APPLICANT: Wang, Hailun
; APPLICANT: Xie, Zhangguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Yajuan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 128
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (99)..(1757)
; OTHER INFORMATION:
; US-10-310-154-128

Query Match      8.2%; Score 103.6; DB 16; Length 2019;
Best Local Similarity 48.8%; Pred. No. 9.8e-20;
Matches 410; Conservative 0; Mismatches 409; Indels 21; Gaps 4;

QY      291 GATGAGAAAGTCAGTAAAGCAATTAAGAGAAAGTCAAGGTTCCAAACCATCCAAATAC 350
      921 GATAGAGAAATCCCTTAAGAGGTTCTCAAGAGGAGAAAGTTATGAGCGTCCCAAG 980
QY      351 TCTACATGCTTTTGCTACAGAGGCAATGACCAAAAACCTCGACGCAAAATTGAGAT 410
      981 GGTGCTGTGTGTAAGTCAAAATTAATCGGAAAGCTTCAGATGCGCGGTGTACAAAG 1040
QY      411 ACATGCGATGAGCAAGCAACCTATTGAATTGGTTCTTGAAAGAGAAAAAGAACTAGACC 470
      1041 AAGGGGATGACGAAAGAGCCATTTAATTCAAGCCGATGAAGG---GAAGTTATTGCC 1097
QY      471 GGTTAAGCCATCGGTGTGCTAGCATGAAGTCTGCTGACAGTGGCGCTTGTCATGTTGGC 530

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Db 1098 GGTCTTGATCGTGTGTTGATGAAATGAAAGAGGCGAGTGTGCTTGTCACAATTCCT 1157
QY 531 TGGGAATTAGCTTATGGG---AAAGAAGAAACCTTTCTTTTCCCAATGTTCCACCTATG 587
Db 1158 CCGTAATATGATGATTTGGTTCACTGAGTCAAGAGGATCTTGTGTTTCCACCTAAC 1217
QY 588 GCAGACTTGTATATGAGTGAAGTATGAGTGTGTTGATGAAACAAAGAGGAGGAAAGCT 647
Db 1218 AGCAGCTATATATATGAGTGAAGTATGAGTGTGTTGATGAAAGAGAGAGTGTGCT- 1272
QY 648 CGAGTATATGACTGTAGAGAAAGAGTGTGTCAGACAGACAGAAAGAAATGATGGG 707
Db 1273 ----GGGACTTGAACATGAAAGAGAGATGAGGCTCTGTAAAGAAAGAGAGG 1328
QY 708 AATTCCTTTTAAAGAGAGAAACCTGAGAGAACCTGCAACATGTAATGAAATGGCCATA 767
Db 1329 AATGACTTGTCAATGGGCAATATGATGAGCTTCCAAAGCATATGAGAGGCTGCC 1388
QY 768 GCATACATGGGGAGCATTTTATGTTTCACTGTATGGAAGTACAGATATGGCTTTA 827
Db 1389 AAGTACATTTAGTACGACACTTGTGATGAGATGAGAGAGCAATCCAG----- 1442
QY 828 GCAGTTAAAAACCATGCTCACTTAACTAGACAGCTTGTCTCACTCAACTAAAAAGATAC 887
Db 1443 CACTGAAAGATCAGCTGCAACCTAAACATGCTGCTGCAAACTGAAATGAAAGATAC 1502
QY 888 GATGAAGCAATGCTCACTGCAACATTTGTGTCAGAGAGAGAGAGAAACCCAAAAAGCA 947
Db 1503 AAGGAAGCTCGCAAGCTTTGCAACCAAGTCTGAACTAGACAGCCAAATGTCAGAGCT 1562
QY 948 CTGTTCAAG 1007
Db 1563 CTCTACAG 1622
QY 1008 TTCCGAAAGGACAAAGATATGCTCTGACAGACAGAGGAGATTAAGAGAGCTACAGCA 1067
Db 1623 ATCAAAAAGGCACTGAAATGATCTGACAGAGAGAGATGCAAGTTGAATTAAGATC 1682
QY 1068 CTTCAG 1127
Db 1683 CTGAAGAGAGAGATCAAGAGAGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1742

RESULT 14
US-10-425-114-13768
; Sequence 13768, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack B.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEO ID NO 13768
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-040-E3_FLI
US-10-425-114-13768

Query Match 8.1%; Score 102.8; DB 13; Length 1617;
Best Local Similarity 50.9%; Pred. No. 1,5e-19;
Matches 329; Conservative 0; Mismatches 302; Indels 15; Gaps 3;
QY 402 TTGAGGATCATGAGATGAG 461

Db 608 TTTGTAAGAGAGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
QY 462 GAACTAGCGGCTTTAGCCATCGGTGCTGACATGAAGTCTGTAAGAGAGAGAGAGAGAG 521
Db 668 GTTATGAG 727
QY 522 CATGTGGCGGGAATTACCTTATG---GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 578
Db 728 AGAGTACACCTGAG 787
QY 579 CCACCTATGAG 638
Db 788 CTCCTAATTTACCGCTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 841
QY 639 GGAAGAGCTGCGAGATATGACTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 698
Db 842 AAGAAATCTTGGGACTTGAAGACCAATATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 901
QY 699 ATGATGAG 758
Db 902 GATGAAG 961
QY 759 ATGAGCATAGATACATGAG 818
Db 962 AAGCTGCAAAATACATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1021
QY 819 ATGCTTTAG 878
Db 1022 AAGGCTCTG-----AAGTCAAGTTCAGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 1075
QY 879 AAGCATAGATGAG 938
Db 1076 AAGAAATACAG 1135
QY 939 CCAAAAGCACTGTTCAAG 998
Db 1136 GTTAAAGCCTTGTACAG 1195
QY 999 CGTATGATTTCCGAAAGGACAAAGATATGCTCTGACAGAGAG 1044
Db 1196 GAGTTGATGTGAG 1241

RESULT 15
US-10-424-599-31694
; Sequence 31694, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEO ID NO 31694
; LENGTH: 2568
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(2568)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_128624C.1
US-10-424-599-31694

Query Match 7.6%; Score 96.6; DB 13; Length 2568;
Best Local Similarity 49.4%; Pred. No. 1.4e-17;

Matches 348; Conservative 0; Mismatches 339; Indels 18; Gaps 3;

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QY 449 AAAAGAGAAAAAAGTAACCGGTTTAGCCATCGGTGTGCTAGCATGAAGTCTGGTGA 508
   |||||
Db 1183 AGATGAGAGAACAAAGTTGATGATGAGCTTGAATAGACTGATATGCTATGAGAGAGGCTGA 1242
   |||||
QY 509 ACGTGCCTTTGTCATGTGCTGCGAATTAAGCTTAATG--GAAAGAGAGAACTTTTC 565
   |||||
Db 1243 GGTTCACCTGTGACCACTGCACCTGAAATATGCTTTGTTCAACAGAGTCCAGCAGCA 1302
   |||||
QY 566 TTTTCCCAATGTTCCACTATGCGACACTGTTATATAGAGTGAAGTATTTGGTTTGA 625
   |||||
Db 1303 GTTGGCTGTAGTCTCTCACTCACTGTTATTTTGAAGTTGAGCTAGTTTCATTGTA 1362
   |||||
QY 626 TGAATCAAGAGAGAGAGAAAGCTGCAATGATGATGAGTGAAGAAAGATGTGACG 685
   |||||
Db 1363 GAAAGAGAGAGAG--TCTTGGGATTTGAACACTGAAGAGAACTTGAAGCTGC 1413
   |||||
QY 686 AGACAGAGAGAGAGAGAGAGATTTCTTTTAAAGAGAGAGAACTGAGAGAGCCAT 745
   |||||
Db 1414 TGGTAAGAGAGAGAGAGAGAGAGATGTTGTTTAAAGCTGTAAGCATGCAAGAGCTTC 1473
   |||||
QY 746 GCAACAGTATGAATGCGCATAGCAATATGCGGAGCAGATTTATGTTTCACTGTATGG 805
   |||||
Db 1474 CAAAAGATATGAAGAGCTGTAAAGTACATAGATATGATTTCTCATTCGTTGAGAGGA 1533
   |||||
QY 806 GAAGTACAGAGATATGCTTTAGCAGTTAAACCCATGCCATGCTTAACATAGCAGCTG 865
   |||||
Db 1534 GAAAAAGCAGGCGCAAGACCTTGAAGTT-----GCCTGCAATCTTAACAATGCTGCTTG 1587
   |||||
QY 866 CCTCATCAAACTAATAAGATACGATGAGCAATTTGTCACCTGCAACATTTGTGTGACAGA 925
   |||||
Db 1588 CAAGTTGAAGTTAAAGACTACAGAGAGAGAGAAATGTGTACCAAGGTGTTAGACCT 1647
   |||||
QY 926 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
   |||||
Db 1648 CGAGAGTACAAATGTTAAAGCCCTCTATAGAGAGGCGCCAAAGCATATATGCAAGTTA 1707
   |||||
QY 986 GATGACCTCAGCAGTATGATTTCCGAAAGGAGCAAAAGATATGCTCTGACGACAGAGC 1045
   |||||
Db 1708 CTTGGATTTGGCTGAACCTTGACATTAAAGAGCTCTTGAGATTTGACCTTAACAAGAGGA 1767
   |||||
QY 1046 GATTAGAGAGAGCTACGAGCACTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1105
   |||||
Db 1768 TGTCAATTTGAGTACAGAGACTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1827
   |||||
QY 1106 AGAAATGTACAGAGAGATTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1150
   |||||
Db 1828 GCATTTTATGAGAAATATGATCAACAAGATGACAAAGATTGGTTC 1872
   |||||
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Search completed: July 7, 2004, 22:27:51
Job time : 833 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2004, 16:21:19 ; Search time 5090 Seconds

(without alignments)
7450.878 Million cell updates/sec

Title: US-09-914-220B-2

Perfect score: 1270
Sequence: 1 gaaagtcgaagggctctc.....atgaagaaggggtacacatca 1270

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_estba: *
3: em_estba: *
4: em_estba: *
5: em_estba: *
6: em_estba: *
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8: em_estba: *
9: em_estba: *
10: em_estba: *
11: em_estba: *
12: em_estba: *
13: em_estba: *
14: em_estba: *
15: em_estba: *
16: em_estba: *
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25: em_estba: *
26: em_estba: *
27: em_estba: *
28: em_estba: *
29: em_estba: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	693.2	54.6	741	13	BU635657 028D02 In
2	673.4	59.4	9	AV784851	AV784851 AV784851
3	649	51.1	669	9	AV823798
4	608.4	47.9	650	14	CB255740 23-E01274

5	490	38.6	892	14	CB981020
6	464.4	36.6	1363	11	AY105475
7	449.6	35.4	972	14	CP436078
8	429	33.8	710	14	CP417393
9	395.6	30.8	839	14	CA765208
10	391.6	30.8	650	10	AW773636
11	380.2	29.9	812	14	CB659598
12	374.8	29.5	705	13	BU67926
13	354.4	27.9	699	13	BO994520
14	341.4	26.9	667	12	BG451848
15	333.4	26.3	493	14	CP23456
16	330.8	26.0	583	10	BE455629
17	326.6	25.7	674	12	BM110915
18	322.8	25.2	471	10	BE209658
19	320.4	25.2	710	12	B566970
20	319	25.1	532	13	BUS77634
21	317.2	25.0	531	13	BO987397
22	312.8	24.5	758	14	CA196409
23	310.6	24.5	813	14	CP430474
24	291.6	23.0	845	14	CB659599
25	290.6	22.9	772	14	CP430421
26	286.4	22.6	358	29	BA97643
27	283	22.3	639	14	CD894285
28	281.6	22.2	661	14	CA185500
29	279	22.0	806	14	CB683163
30	276.4	21.8	469	10	AW22544
31	274	21.6	380	29	BA97644
32	271.8	21.4	538	13	BU878153
33	264.4	20.3	645	10	BF646472
34	258.2	20.8	812	28	BH557130
35	255.6	20.1	483	9	AU225473
36	252.6	19.9	479	10	AW428872
37	248	19.5	490	12	BG462802
38	247	19.4	705	14	CD207807
39	246	19.4	655	14	CD883248
40	243.6	19.2	557	10	AW441601
41	240.6	18.9	648	13	CA120169
42	240.6	18.9	445	12	BG553433
43	239.2	18.8	636	9	AV925548
44	237.2	18.7	738	13	CA081013
45	236.8	18.6			

ALIGNMENTS

CB981020 CAB70003-
AY105475 Zea mays
CP436078 EST672423
CP417393 USDA-FP 1
CA765208 AF53-RF
AW773636 EST332622
CB659598 OSJUNC16L
BU67926 M106A06 P
BO994520 QGF7H10.Y
BG451848 NF10101D
CP23456 PtaXoXoXo
BE455629 HVSMG001
BM110915 EST558451
BE209658 scj31910.Y
B566970 B566970
BUS77634 BA90002.
BO987397 QGF12B22.
CA196409 SCBPAD108
AV916516 AV916516
CP430474 PHL 28 P0
CB659599 OSJUNC16L
CP430421 PHL 28 P0
BA97643 Arabidops
CD894285 G118.1250
CA185500 SCSPST307
CB683163 OSJUNC16L
AW22544 EST299355
BA97644 Arabidops
BU878153 V043G04 P
BF646472 NF075D06E
BH557130 BOGMM71TF
AU225473 AU225473
AW428872 LjJmpeest
BG462802 EM1_45_G0
CD207807 HSL_35_C1
CD883248 F1.112L08
AW441601 EST10997
CA120169 SCCCLR107
BG553433 BA957C05.
AV925548 AV925548
CA081013 SCACAM204

RESULT 1
BU635657
LOCUS
DEFINITION 741 bp mRNA linear EST 23-SEP-2002
028D02 Infected Arabidopsis Leaf Arabidopsis thaliana CDNA, mRNA
SEQUENCE.
ACCESSION BU635657 GI.23302912
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1 (bases 1 to 741)
Lundgaard, M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.
and Welinder, K.G.
EST sequencing of Erysiphe cichoracearum infected Arabidopsis
plants
JOURNAL
COMMENT
Unpublished (2002)
Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
Solngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk.
Location/Qualifiers
FEATURES

source

1. .741
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia"
/db_xref="taxon:3702"
/dev_stage="Plant 3 weeks old, three days post infection"
/clone_lib="Infected Arabidopsis leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. choroacearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dt selected."

ORIGIN

Query Match 54.6%; Score 693.2; DB 13; Length 741;
Best Local Similarity 99.4%; Pred. No. 1.2e-164;
Matches 732; Conservative 0; Mismatches 8; Indels 4; Gaps 3;

222 CGTTGTCATAGTGGCCATCTCAGAGGGTAATGTTCTCCTAAAGTTGATGTAAGCT 281
Db 1 CGTTGTCATAGTGGCCATCTCAGAGGGTAATGTTCTCCTAAAGTTGATGTAAGCT 58

QY 282 GAGGCTTTGATGAGAAAGTCAGTAAGCAATTATTAAGAGAGGTCACGGTTCCAAACCA 341
Db 59 GAGGCTTTGATGAGAAAGTCAGTAAGCAATTATTAAGAGAGGTCACGGTTCCAAACCA 118

QY 342 TTCAGAGTCTCATGCTTTTGTCTACACAGGCGCATGAGCAAAAACCTGCGACACAA 401
Db 119 TTCAGAGTCTCATGCTTTTGTCTACACAGGCGCATGAGCAAAAACCTGCGACACAA 178

QY 402 TTTGAGGATACATGCGACATGAGCAACAATTGAATTGTTCTTGGAAAAAGAAAAA 461
Db 179 TTTGAGGATACATGCGACATGAGCAACAATTGAATTGTTCTTGGAAAAAGAAAAA 238

QY 462 GAAGTACCGGTTTATGCGATGGTGTCTGACATGAAGTCTGTAAGTGGCTTGTG 521
Db 239 GAAGTACCGGTTTATGCGATGGTGTCTGACATGAAGTCTGTAAGTGGCTTGTG 298

QY 522 CATGTTGGCTGGGAATTAGCTTATGGAAGAAAGAAATTTTCTTCCCAATGTTCCA 581
Db 299 CATGTTGGCTGGGAATTAGCTTATGGAAGAAAGAAATTTTCTTCCCAATGTTCCA 358

QY 582 CCTATGCGACATTTGATATAGAGTGAAGTTATGGGTTTGAATGAACAAAGAGGA 641
Db 359 CCTATGCGACATTTGATATAGAGTGAAGTTATGGGTTTGAATGAACAAAGAGGA 418

QY 642 AAAGCTGCGATGATATGATCTGTAGAGAAAGATTGGTGCAGACAGCAAGAAAAATG 701
Db 419 AAAGCTGCGATGATATGATCTGTAGAGAAAGATTGGTGCAGACAGCAAGAAAAATG 478

QY 702 GATGGAATTCTCTTTTAAAGAGAGAACTGAGGAGGCATGCAACAGTATGAATG 761
Db 479 GATGGAATTCTCTTTTAAAGAGAGAACTGAGGAGGCATGCAACAGTATGAATG 538

QY 762 GCCATAGCATATCATGAGGAGAGATTTTATGTTTCAGCTGTATGGAAGTACAGAGATATG 821
Db 539 GCCATAGCATATCATGAGGAGAGATTTTATGTTTCAGCTGTATGGAAGTACAGAGATATG 598

QY 822 GCTTTAGCAGTTAAAAACCATGCGATCTTAACTAGCAGTGGTCCCTCATC-AACTAAA 880
Db 599 GCTTTAGCAGTTAAAAACCATGCGATCTTAACTAGCAGTGGTCCCTCATC-AACTAAA 658

QY 881 ACGATAGAGTAACCAATTGGTCACTGCAACATGTTGTGACAGAAAGAGAAAAACC 940
Db 659 ACGATAGAGTAACCAATTGGTCACTGCAACATGTTGTGACAGAAAGAGAAAAACC 717

QY 941 AAAAGCACTGTTCAAGAGAGGAA 964
Db 718 AAAAGCACTGTTCAAGAGAGGAA 741

RESULT 2
AV784851/c

LOCUS AV784851 694 bp mRNA linear EST 28-MAR-2002
DEFINITION AV784851 RAFL6 Arabidopsis thaliana cDNA clone RAFL06-08-N18 3',
mRNA sequence.
ACCESSION AV784851
VERSION AV784851.1 GI:19803641
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Bukharoyea; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 694)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishi,Y.,
Arakawa,T., Shibata,K., Shingawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
TITLE Unpublished (2002)
JOURNAL Contact: Motoaki Seki
COMMENT Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a 5'UTR/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for
further details.

FEATURES

source

1. .694
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL06-08-N18"
/dev_stage="Plants at various developmental stages from germination to mature seeds"
/lab_host="DH10B"
/note="Site 1: SctI; Site 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN

Query Match 53.0%; Score 673.4; DB 9; Length 694;
Best Local Similarity 99.7%; Pred. No. 1.2e-159;
Matches 685; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 584 TATGCGACATTTGATATAGAGTGAAGTTATTTGGTTTGAATGAACAAAGAGGAAA 643
Db 694 TATGCGACATTTGATATAGAGTGAAGTTATTTGGTTTGAATGAACAAAGAGGAAA 635

QY 644 AGCTCGAGTATATGATCTGTAGAGAAAGATTGGTGCAGCAGACAGAAAGAAATGCA 703
Db 634 AGCTCGAGTATATGATCTGTAGAGAAAGATTGGTGCAGCAGACAGAAAGAAATGCA 575

QY 704 TGGGAATTCTCTTTTAAAGAGAGAACTGAGGAGGCATGCAACAGTATGAATGGC 763
Db 574 TGGGAATTCTCTTTTAAAGAGAGAACTGAGGAGGCATGCAACAGTATGAATGGC 515

QY 764 CATAGCATATGAGGAGAGCATTTTATGTTTCAGCTGTATGGAAGTACAGAGATATGGC 823
Db 514 CATAGCATATGAGGAGAGCATTTTATGTTTCAGCTGTATGGAAGTACAGAGATATGGC 455

QY 824 TTTAGCAGTTAAAAACCATGCGATCTTAACTAGCAGTGGTCCCTCATCAACTAAAACG 883
Db 454 TTTAGCAGTTAAAAACCATGCGATCTTAACTAGCAGTGGTCCCTCATCAACTAAAACG 395

QY 884 ATACGATGAAGCAATTGGTCACTGCAACATGTTGTGACAGAAAGAGAAAAACCATA 943
Db 394 ATACGATGAAGCAATTGGTCACTGCAACATGTTGTGACAGAAAGAGAAAAACCATA 335

Query Match	51.1%	Score 649	DB 9	Length 669
94	AGCACTGTTCCGAAAGAGGAAAAGCAAAAGCAGAGCTTAGACACAGATGCACTGACACGCGA	1003		
334	AGCACTGTTCCGAAAGAGGAAAAGCAAAAGCAGAGCTTAGACACAGATGCACTGACACGCGA	275		
1004	TGATTTCCGAAAGAGCACAAGATATGCTCTGACGACCAAGGCGATTAGAAAGAGACTACG	1063		
274	TGATTTCCGAAAGAGCACAAGATATGCTCTGACGACCAAGGCGATTAGAAAGAGACTACG	215		
1064	AGCACTTGACAGACAGCAAGAAAGCCTTGTACCAAAAGCAAGAAATGTACCAAGGAAAT	11233		
214	AGCACTTGACAGACAGCAAGAAAGCCTTGTACCAAAAGCAAGAAATGTACCAAGGAAAT	155		
1124	ATTCAAGAGGAAAGATGGAAGGCGGCTAA-GTCAAAAGAGCCTTTTGGTGTAGTAGCT	1182		
154	ATTCAAGAGGAAAGATGGAAGGCGGCTAAAGGCTTTTGGTGTAGTAGT	95		
1183	TATGCAATGGTTGTTCCCTTTCTCCGATCTTTCGACGCCACAGATTAAAGCAG	1242		
94	TATGCAATGGTTGTTCCCTTTCTCCGATCTTTCGACGCCACAGATTAAAGCAG	35		
1243	ATTAAATGTATGAAGAGGTTCAATT	1269		
34	ATTAAATGTATGAAGAGGTTCAATT	8		
RESULT 3				
AV823798	AV823798	669 bp	mRNA	linear
LOCUS	AV823798	RAFL6	Arabidopsis thaliana	CDNA clone RAFL06-08-N18 5',
DEFINITION	RAFL6	Arabidopsis thaliana	CDNA clone RAFL06-08-N18 5',	
ACCESSION	AV823798			
VERSION	AV823798.1	GI:19865858		
KEYWORDS	EST.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 669)			
AUTHORS	Seki, Y., Nakasaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arkawa, T., Shibata, K., Shingawa, A., Morimatsu, M., Hayashizaki, Y. and Shinohara, K.			
TITLE	Large scale analysis of Arabidopsis full-length cDNA (2002b)			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: msekic@rcc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified Bluescript vector as a SctI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/Plant/index_e.html) for further details.			
FEATURES	Location/Qualifiers			
SOURCE	1..669			
	/organism="Arabidopsis thaliana"			
	/mol_type="mRNA"			
	/db_xref="taxon:3702"			
	/clone="RAFL06-08-N18"			
	/dev_stage="plants at various developmental stages from germination to mature seeds"			
	/lab_host="DH10B"			
	/clone_11b="RAFL6"			
	/note="Site 1: SctI; Site 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"			

[illegible]

COMMENT

Contact: Weishaar B
 ADIS DNA core facility at MPiZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 650 Std Error: 0.00
 Plate: 7 row: M column: 05
 Seq primer: T7R: CTAATGCACTCATATAGGA.
 Location/Qualifiers

FEATURES

Source

1..650
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /cultivar="Eifel-2 (Ei-2)"
 /db_xref="GABI:592595"
 /db_xref="taxon:3702"
 /clone="MPiZp772M0570"
 /tissue_type="whole plant"
 /dev_stage="adult plant, mixed stresses"
 /lab_host="E. coli TOP10"
 /clone_lib="MPiZ-ADIS-027"
 /note="Vector: pSPORT1; Site1: SalI; Site2: NotI; cDNA library from Arabidopsis thaliana, accession Eifel-2; ten week old total plants grown under long-day conditions in soil, whole adult plants were treated for 24 hours with different stresses, (1) at 4M-0 C in the dark, (2), at 37 Grad C in the dark, (3) lying in the lab after removing from soil, (4) in the greenhouse after wounding leaves with a forceps, (5) in the lab watering with a 150 mM NaCl solution, (6) at 26 M-0C in the light/UV; equal quantities of stressed plant material were pooled; library was made at the Max-Planck-Institute for Plant Breeding Research, Cologne, Germany; cloning sites SalI-NotI, primer sites and orientation:
 T7-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-SP6. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund I: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection', PI: Bernd Weishaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 47.9%; Score 608.4; DB 14; Length 650;
 Best Local Similarity 98.1%; Pred. No. 3.5e-143;
 Matches 626; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 46 ATTATCTCTCGTCGATCCAGTCTTGTGAGTGAATTCGACGACGAGTCAC 105
 DB 13 ATTATCTCTCGTCGATCCAGTCTTGTGAGTGAATTCGACGACGAGTCAC 72
 QY 106 TACTCTTGAAGCTTCTCAATCTTCCACGAGTTGATTTGGAAATATGATGAA 165
 DB 73 TACTCTTGAAGCTTCTCAATCTTCCACGAGTTGATTTGGAAATATGATGAA 122
 QY 166 GAGATCAAACTCAAGACATGACCAAGAGCGAAATGTTACTGAAGAGCCGCT 225
 DB 133 GAGATCAAACTCAAGACATGACCAAGAGCGAAATGTTACTGAAGAGCCGCT 192
 QY 226 GTGCATAGTG-GCCATCTCAAGAGGTAATGTTCTCTTAAAGTTGATGTAAGCTG 284
 DB 193 GTGCATAGTGAGCATCTCAAGAGGTAATGTTCTCTTAAAGTTGATGTAAGCTG 252
 QY 285 GTCTTGATGAGAAAGTCAAGTATTAAGAGAGGTCACGGTTCCAAACCATCC 344
 DB 253 GTCTTGATGAGAAAGTCAAGTATTAAGAGAGGTCACGGTTCCAAACCATCC 312
 QY 345 AAGTACTTACATGCTTTTGTCACTACAGGCGACATGACCAAACTCGCAGCAATTT 404
 DB 313 AAGTACTTACATGCTTTTGTCACTACAGGCGACATGACCAAACTCGCAGCAATTT 372

QY 405 GAGATACATGCGATGAGACGCAACCTATGTAATGTTCTTGAAAAAGAAAAAGAA 464
 DB 373 GAGATACATGCGATGAGACGCAACCTATGTAATGTTCTTGAAAAAGAAAAAGAA 432
 QY 465 CTAGCCGGTTTACCATCGGTGTTGCTTACGATGAAGTCTGTGACGCTTGTCAT 524
 DB 433 CTAGCCGGTTTACCATCGGTGTTGCTTACGATGAAGTCTGTGACGCTTGTCAT 492
 QY 525 GTTGGCTGGGAATTAAGTATGGAAGAGAAACCTTTTCTTTCCAAATGTTCCACCT 584
 DB 493 GTTGGCTGGGAATTAAGTATGGAAGAGAAACCTTTTCTTTCCAAATGTTCCACCT 552
 QY 585 ATGCACAGACTTGTATATGAGTGAAGTAAATTTGGTATGAAACAAAGAGGAAAA 644
 DB 553 ATGCACAGACTTGTATATGAGTGAAGTAAATTTGGTATGAAACAAAGAGGAAAA 612
 QY 645 GCTCGAGTGAATGACTGTAGAGGAAGGATTTGTC 682
 DB 613 GCTCGAGTGAATGACTGTAGAGGAAGGATTTGTC 650

RESULT 5

CB981020

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Expressed sequence tags from cabernet sauvignon berries at various developmental stages
 Unpublished (2003)
 Contact: Douglas Cook, PhD
 CAES Genome Facility
 UC Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: dcook@ucdavis.edu
 Seq primer: GCCAAGCATGCTTAG.
 Location/Qualifiers

FEATURES

Source

1..892
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultivar="Cabernet Sauvignon"
 /db_xref="taxon:29760"
 /clone="CAB70003 IVAR_F02"
 /sex="Hermaphrodite"
 /dev_stage="Post-Veraison, 18-19 brix"
 /lab_host="DH5alpha"
 /clone_lib="Cabernet Sauvignon Berry Post-Veraison - CAB7"
 /note="Organ: Berry; Vector: pDNR; Site 1: SfiI; Site 2: SfiI; CAB7 is a cDNA library of Cabernet Sauvignon Clone 8 berries. Samples were collected post-veraison from field-grown vines during stage III of berry growth at 89 days after full bloom. Berries soluble solid concentration ranged between 18-19 brix. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directly cloned. 5' and 3' adaptors were used in cloning as follows: 5'-AAGCAGGATGACCAAGGAGGCGCATTAACGGCGG-3' and 5'-ATTCTAGAGCGGAGGCGGCGGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 38.6%; Score 490; DB 14; Length 892;
 Best Local Similarity 77.0%; Pred. No. 3.7e-113;
 Matches 609; Conservative 0; Mismatches 181; Indels 1; Gaps 1;

163 CTGAGCATCAAACTCAACATGACGAGAGAGCAAAATGTTACTGAAGAGTGC 222
 101 CTGCAAGATGCAAAACCTGATCAGAGAGAGAAATGATTTACTGAAATGACGA 160
 223 GTTGTGATGATGGCCATC-TCAAGAGGTAAAGTCTCTTAAGTGAATGAGAGCT 281
 161 TTGTGTGATGGGAACTCTTCAAGATGATGCGGTCTCTCAAAAGTTGATTCGAAGTG 220
 282 GAGCTTTGATGAGAAAGTCAGTAAAGCAATTTAAAGAAAGGTCAAGTTCGAACCA 341
 221 GAGTTTCTTCAAGAAAGTCACAAACATCTGAAAGAGTCAATGTCAGAAACCA 280
 342 TCCAAAGTCTCAATGCTTTTGTCTACTAGAGGAGTGAACCAAACTGCGACACAAA 401
 281 TCCAAATACCTCAACATGTTCTTGTCAATAGCGGAGTGAAGTGAACACCCAGCAG 340
 402 TTGAGAGTACATGAGCATGAGCAGCAACTTATGATTTGTTCTGAAAAAGAAAAA 461
 341 TTGAAAGACATGAGAAATGAACACGTCAGTTGAAATAGCATAGAAAAAGAAAAA 400
 462 GAACTAGCCGATTTAGCATCGGTGTTGCTAGCATGAAGTCTGTAAGTGGGCTGTG 521
 401 GAAATGACGGGATTTGGCTATTTGGTGTCTCCAAACATGAGTGTGTAAGTGGCTTTTA 460
 522 CATGTTGGCTGGAAATAGCTTATGAGAAAGAAAGAACTTTTCTTTCCAAATGTTCA 581
 461 CATGTGGGTTGGGAATTTGGGCTATGGGAAGAAAGAAAGTTTCTTTCCGAAATGTTCCG 520
 582 CCTATGGCAACCTGTTATATGAGGTGAAAGTTTGGGTTTGTATGAACAAAGAGAGGA 641
 521 CCTATGGCAACATTTTGTATGAGGTGAAAGTTTGGCTTTGATGAACTTAAAGAGGGG 580
 642 AAAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 701
 581 AAAGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 640
 702 GATGGAAATCTCTTTTAAAGAGAGAACTGAGAGAGCCATGCAACAGTATGAATG 761
 641 GATGAAATGTTTACTTCAAGAGAGAAACTGAGAGAGGCTATGCAACAGTATGAATG 700
 762 GCCATGACATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 821
 701 GCCATGACATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 760
 822 GCTTTGACATTAATAAACCAGTCCATTAACATGACAGCTTGCCTCACTAAACTAAA 881
 761 GCTTTGCTGTGAAGATTCATGACCTTAAACATGAGAGATGCTGATTAAGCTGAAG 820
 882 CGATACGATGAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAACCA 941
 821 CGCTAGCAAAAAAGCAATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAAAC 880
 942 AAAGCACTGTT 952
 881 AAGGCACTTATT 891

RESULT 6
 AY105475 1363 bp mRNA linear HTC 16-OCT-2002
 LOCUS Zea mays
 DEFINITION Zea mays PCO126622 mRNA sequence.
 ACCESSION AY105475
 VERSION AY105475.1 GI:21208553
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD

REFERENCE 1 (bases 1 to 1363)
 AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitelitt,M.S.,
 Arthur,I.W., Hanafey,M., Morgante,M. and Tingey,S.V.
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes
 JOURNAL Unpublished (2002)
 REFERENCE 2 (bases 1 to 1363)
 AUTHORS Coe,E.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 COMMENT If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.

FEATURES
 source
 1..1363
 /organism="Zea mays"
 /mol_type="mRNA"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/Dupont Consensus
 Library"
 /note="this sequence is part of a project of EST
 assemblies resulting from the application of public
 contigs to seed Dupont contigs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

ORIGIN
 Query Match 36.6%; Score 464.4; DB 11; Length 1363;
 Best Local Similarity 71.6%; Pred. No. 1.2e-106;
 Matches 637; Conservative 0; Mismatches 251; Indels 2; Gaps 2;

237 CCATCTCAAGAGGATATGTTCTCTTAAGTGAATGAGAGCTGATGTTGATGAG 296
 222 CTTCCCCAGATGCGCCGCCACCGTGTCTCTGACATGAGGCCCTTCAAGC 281
 297 AAGTCATGAAGAGATTTTAAAGAGGTCACGTTCCAAACATCCAGTACTATCA 356
 282 AAGCTTAAGAGAAATCATCAAGAGGTCATGAGAGAACCGTGAAGTTCGAGAG 341
 357 TGCTTTGTCACTACAGGCGATGACCAAACTCGACACCAATTTGAGATACATG 416
 342 TGCTTTGTGACATATGAGCATGATGATGATGATGATGATGATGATGATGATG 401
 417 CATGACAGCAACTTATTAATGTTGTTTGAAGAAAGAAAGAAAGAACTACCGGTTTA 476
 402 CAAGACCAATCCCAATTAATTAATGTTGAAGAAAGAAAGAAAGAAAGTCTGTTTA 461
 477 GCATGCGTGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 536
 462 GGCATGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 521
 537 TTAGCTTAAGAGAGAAAGAAAGAACTTTTCTTTCCCAATGTTCACTATGAGAGCTG 596
 522 CTAGGCTATGCAAGAGAGAAAGTTTTCATTCCTCCAAATGTCTCTCAATGAGAGCTT 581
 597 TTATATGAGTGAAGTATATGAGTTTGAAGAAAGAAAGAGAGAAAGCTGCAATGAT 656
 582 GTTATGAAGTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 641
 657 ATGACCTGTAGAGAAAGATTTGCTGACAGACAGAAAGAAAGATGATGATGATGAT 716
 642 ATGACAGTTGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 701
 717 TTAAAGAGAGAAAGCTGAGAGAGAGCTGCAACAGTATGAATGAGCTTACATACATG 776

Db	702	TTCAAAGAAAGAAAGCTTGAGAGAGGCCATTGCAGCAATATGAAATATGGCAATTGCATACATG	761
Qy	777	GGGAGCATTTTATGTTTCAGCTGTATGGGAATGCCAGATATGGCTTTAGCACTTTAA	836
Db	762	GGAGATGATTTCAATGTTTCAATTTATTTGGAAAGTACAGAGCATAGGCTTGGCTGTGAAA	821
Qy	837	AACCCATGGCCATTTAATATAGCAGCTTGCTCATCAATCAATCAAAACGATATGATGAAACA	896
Db	822	AATCATGCGCATCTTCATATATGCTGCAATGCTGATCAAACTPAAGAGATTTGATGAACTT	881
Qy	897	ATTGGTCACTCCAACTATGTGTGTGCAGAGAAGAGAAAGAAACCCAAAGCACTGTTTCA	956
Db	882	ATTGGCGAGTGAATGATTTGTTTGCACAGAAATGAAATTAATGTCAAAGCCGTGTTGAG	941
Qy	957	AGAGGGAAGCAAAAGGACAGCTAGACAGATGAGCTCAGCACTGATGATTTCCGAAAG	1016
Db	942	CGAGGAAAGGCTAAATCTGAACCTTGCCAGACAG - ACAGGAGGGAAGATTTCTCAA	1000
Qy	1017	GCACAAAAGTATGCTCTGACAGCAGAGCGATTTAGAAAGAGCTTACAGCACTTGCAGAG	1076
Db	1001	GCGAAGAAAGTACTCCCCAGAAAGACAGAGATCAATTCGGAGAGCTCCGTTTGCTGCCGGA	1068
Qy	1077	CAAGGAAGCCTGTACCAAAAGCAGAAAGAAATGTCAAAAGGAATTT	1126
Db	1061	CAAGCAAGGACTT - TACCAAGAGCAGAAAGAGCTTACAAAGGCTCTCTT	1109

RESULT 7	CF436078	LOCUS	DEFINITION
	CF436078	972 bp	mRNA
	EST672423	normalized cDNA library of onion <i>Allium cepa</i>	linear EST 04-SEP-2003

ACCESSION	CF436078	GI:34458768
VERSION	CF436078.1	
KEYWORDS	EST.	
SOURCE	Allium cepa	(onion)
ORGANISM	Allium cepa	

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
Allium.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 972)	Hayes, M.J., Cheung, F., Van Aken, S., Uterback, T. and Town, C.D.	Expressed Sequence Tags from a normalized library of mixed onion tissues (<i>Allium cepa</i>)

**JOURNAL,
COMMENT**

Department of Horticulture
USDA-ARS and University of Wisconsin
1575 Linden Drive, Madison, WI 53706, USA

Email: mjhavey@facstaff.wisc.edu
TIGR sequence name ACACD15TR. For more information:
<http://havey1ab.hort.wisc.edu>
Seq primer: CAG GAA ACA GGT ATG ACC.

FEATURES	Location/Qualifiers
source	1. .972

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/organism="Allium cepa"
/mol_type="mRNA"
/cultivar="Red Creole (bulbs), unknown (callus), Ebano &
Texas Legend (roots)"
/db_xref="taxon:4679"
/clone="ACACD15"
/tissue_type="Callus, roots, and young bulbs"
/clone_lib="normalized cDNA library of onion"
/notes="vector: pCMVSPORT.1-cdbd (Invitrogen); Site 1:
EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA
from callus, roots, and young bulbs were combined to
synthesize the library. Normalization to enrich for
low-copy transcripts was performed by proprietary
techniques of Invitrogen."
```

Query Match	35.4%;	Score 449.6;	DB 14;	Length 972;
Best Local Similarity	70.0%;	Pred. No. 6.5e-103;		
Matches 619;	Conservative 0;	Mismatches 264;	Indels 1;	Gaps 1

QY	181	ACACATGACCAAGAGAGGAAATAGTTTCTGTGAAGAGATGCGCTGTGCATAGT- <i>GC</i> CA	239
Db	80	ACTGACCGGAAAGAGATGATATTTGTTACACAGACATGTGCTTTGTACATCGAGACCA	139
QY	240	TCTCAAGAGGGTAATGTTCTCTTAAAGTTAGTAGAAGCTGAGGTCTTGATGAGAA	299
Db	140	CTTCAGATGAAAAATGAGCCACCACAGGTGCATCAGAGCTAGAGATCAGATCCCTTCATAGAAA	199
QY	300	GTCAGTAGCAGATATATTAAGAGAGTCACGGTTCCAAACCATCCAGATCTACATGAC	359
Db	200	GTCATAAAGCAATATTCATAAAGAGGGCATGGAACAAAGCCATCAACATCAGCAACATGC	259
QY	360	TTTTGTCACTACAGGGCATGAGACCAAAATCTGCAGCACAAATTTGAGATACATGCAAT	419
Db	260	TTCTTACATTCACAGAGATGGGTCAAGAGAACTTTGCACAAATTTGAAAGATACATGGCTA	319
QY	420	GAGCAGCAACTATTTGAAATTGGTCTTGGAAGAGAAAAAGAACTAGCCGGTTTAGCC	479
Db	320	GAAACAACACCTTTTGAACCTGTGTTTAGAGAAAGAAAAAGAAATGCGGCGCTTGCC	379
QY	480	ATCGGTGTTGATGATGATAGCTGAGTGAAGCGTGCTTGTCATGTTGGCTGGGATTA	539
Db	380	ATTGAGATTGCAGATGAGAGAGTGGAGCGTGCATGTTTAAATGTTGGAATGGAATTA	439
QY	540	GCTTATGAGAAAGAGAAACCTTTTCTTTCCCAATGTTCCACTATGGCAGACTTGTTA	599
Db	440	GGATATGGGGAAGAGGCAATTTCTCTTCCCAATGTGCCTCCGCTGCAGATTTGATTA	499
QY	600	TATGAGGTGGAAGTATTTGGTTGATGAACAAAGAGGGGAAAAAGCTGCAGTATATG	659
Db	500	TATGAGATTGAGCTGATTTGTTTGATATATCAAGAGAGGAGAGCTTAGAGTGCATG	559
QY	660	ACTGTAGAGGAAAGGATTTGTGCAGACAGACAGAAAGAAATGATGGGAATTCCTTTT	719
Db	560	ACAGTAGAGGAAAGAAATGAAAGCAGACAGAGAAAGAAAGCTAGAGGTAACTAACCTTC	619
QY	720	AAGAGAGGAAACTGGAGAGAACCATGCACAGTATGAATATGGCCATATGACATACATGGG	779
Db	620	AAGAGGAAAACTTGAAGAGGCTATGCAACATATGAAATGGCCATATGCAATATATGGA	679
QY	780	GACGATTTTATGTTTCACTGTATGGGAATGACAGATATGCGCTTTAGAGTTAAAAAC	839
Db	680	GATGATTTCAATGTTCCAGTTATTTGGAAGATACAGACATGCGCTCTGAATGTGAAAAAT	739
QY	840	CCATGCCACTTAAATACATAGCAGCTTGCCCTCATCAAACTPAAACGATACGATGACGAAT	899
Db	740	CCATGTCAATCCACATGCGTGTCTGCTTAATTAAGCTTAAGCGATATGCAAGATGCCAT	799
QY	900	GGTCACTGCAACATTTGTGTGACAGAAAGAGAAAAACCCAAAGACCTGTTCCAGAGA	959
Db	800	GGTCAATGATCTGTGTACTATCAGAAAGACGAGAAATGTGTAAGCCCTTAATTCAGGCT	859
QY	960	GGAAGAGCAAGGCGAGACTAGAGCAGATGCACTGAGCACGTGATGATTTCCGAAAGCA	1019
Db	860	GGAAGAAAGCAAGTCGAGCTTGGAACAGATAGAGTCTGCTCGAGAGGACTTTGAAAGAGCA	919
QY	1020	CAAAAGTATGCTCTCTGAGCAAGGCGCATTAAGAAAGCTPACG	1063
Db	920	CAAAATATTTTCCCCATGACAGAGCTATTTATTAAGAGATGAAG	963

RESULT 8	
CF417393	
LOCUS	710 bp mRNA linear EST 02-SEP-2001
DEFINITION	USA-FP 155000-333 Citrus sinensis: Insect-damaged immature leaves/stems from field collected Valencia orange Citrus sinensis
ACCESSION	CNA clone IDPL-004_G02 5', mRNA sequence.
VERSION	CF417393.1 GI:34418520

KEYWORDS	EST.
SOURCE	Citrus sinensis
ORGANISM	Citrus sinensis
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosidae; euroside II; Sapindales; Rutaceae; Citrus. 1 (bases 1 to 710)
AUTHORS	Shatters, R.G. Jr., Chaparro,J.X., Bausher,M.G., Hunter,W.G. and Niede,Z.R.P.
TITLE	Expressed Sequence Tags from Insect-Damaged Field-Collected Sweet Orange (<i>Citrus sinensis</i> (L.) Osbeck) Immature Leaves and Stems Unpublished (2003)
JOURNAL	Contact: Shatters, Jr. RG Subtropical Insects Research Unit USA, ARS, U. S. Horticultural Research Laboratory 2001, South Rock Road, Fort Pierce, FL 34945, USA Tel: 772 462 5912 Fax: 772 462 5986 Email: rebatters@usuhrl.ars.usda.gov Seq primer: T3 Primer.
FEATURES	Location/Qualifiers 1..710
SOURCE	/organism="Citrus sinensis" /mol_type="rRNA" /cultivar="Valencia" /isolate="mixed field population" /db_xref="taxon:2711" /clone="IDFL-004 G02" /issue type="Flush leaves and stems" /clone.lib="Citrus sinensis; insect-damaged immature leaves/stems from field collected Valencia orange" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Citrus sinensis (L.) Osbeck; Standard library construction protocols from StrataGene cDNA synthesis kit (cat.# 200401-5) and Uni-ZAP XR vector kit (cat.# 237211) were followed using poly(A) RNA."
ORIGIN	
Query Match	33.8%; Score 429; DB 14; Length 710;
Best Local Similarity	76.5%; Pred. No. 1e-97;
Matches	Conservative 0; Mismatches 165; Indels 1; Gaps 1;
Db	423 CAGCAACTTATTGAATGGTTCTTGGAAGAAGAAAAAAAGAACTAGCCGTTTAGCCATC 482 1 CAACAACCGCTGGAATGTTTAGAAGAAAAGAAAAAGAGATGACTGCCTGGCTATT 60
QY	483 GGTTGTGTACATGAAGTCGTGTGAAGTCGCCCTGTGCATGTTGGCTGGGAATTGACT 542 61 GGGGTGTACACATGAAGGCTGTGTGAACATGACTGTACATGTGTGGCTGTGGAAATGGGT 120
Db	543 TATGGAAAGAAAGAAACTTTTCTTTTCCCATGTTCACCTATATGGCAGACTTGTTATAT 602 121 TATGGAAAGAAAGAAAGCTTTCTTTCCCAATGTGTCTCCATGTGCAGACTTAGTATAT 180
QY	603 GAGGTGGAAGTTATTTGGTTTGATGAACAAGAGAGGAAAAAGCTCGAGTGATATGACT 662 181 GAGGTGTGTGCATATGGCTTTGACGAACCAAGAGAGGAAAAAGCTGTATGACATGACT 240
Db	663 GTTAAGAAAGAGATTGTGTGCAGCAGACAGAAAGAAAAAATGATATGGAAATTCCTTTTAA 722 241 GTCAAGAAAGAAAGATTGTGTGCAGCAGACCAGAAAGAAAGATGAGAAATGCTTATTATAAG 300
QY	723 GAGAGAAAGCTGAGAGAACCATGCAACAGTATGAATGGCCAATGACATATGAGGAGAC 782 301 GAGAGAAAGCTGAGAGAACCATGCAACAGTATGAATGGCCAATGACATATGAGGAGAC 360
Db	783 GATTTATGTTTCAGCTGTATGGGAAGTACAGATATAGCTTTAGCAGTTAAAAACCA 842 361 GACTTCATGTTCCAGTTGTTGGGAAGTACCGGAGTATAGCTTTGAGTTAAGATCA 420
QY	843 TGCCATCTTAATATAGAGCTTTGCTCTATCAAACTAATAAGATATGAAGCAATTGGT 902 421 TGCCATCTTAATATAGAGCAATGCTATTAAGTCAAAAGCTTTATGAAGAGCCATGGG 480

Qy	903	CACGCAAACTTGGCTTGACAGAAAGAGAGAAAAACCCAAAGCACTGTTCCAGAAAGGG	962
Db	481	CAATGCAGCCTTGTTATTGGAGAGATGAAAATATATGTGAAGGCCCTTTTCAGACAGGA	540
Qy	963	AAAGCAAGGCAGAGCTTAGACAGATGAGTCTCAGCACGTGATGATTTCCGAAAGSCAA	1022
Db	541	AAGCTTAGACAGAACTTGGGCAAAAGATGCTGCCGGGAAGCTTTCTTAAGAGCAGGT	600
Qy	1023	AAGTATGCTCTGACGACAAAGGCGATTGA-AGAGAGCTACGACACTTGCAGAGCAAGA	1081
Db	601	AAATTTCACCTTGAAAGCAATCAATTGACAGGGAGACTTCGTTTGCTCGCTGAACATGA	660
Qy	1082	GAAGCCTTGATCAACAAAGCAGAAAGAAATGTACAAAGATATT	1126
Db	661	AAAGCTGTATACAGAGCAAAAGAGATCTATAGAAATTTT	705
RESULT 9			
LOCUS	CA765208	839 bp	mRNA linear EST 08-JAN-2003
DEFINITION	CA765208	AF53-Rpf_06_K05_T7_029.ab1	IRRI Drought Stress Panicle Library
LOCUS	Oryza sativa	(Indica cultivar-group)	cDNA clone C0002165 5' similar to 70 kDa peptidylprolyl isomerase (EC 5.2.1.8) (Peptidylprolyl cis-trans isomerase) (Cyclophilin) (PPIase), mRNA sequence.
ACCESSION	CA765208		
VERSION	CA765208.2	GI:27546946	
KEYWORDS	EST.		
SOURCE	Oryza sativa	(Indica cultivar-group)	
ORGANISM	Oryza sativa	(Indica cultivar-group)	
REFERENCE	Bukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.		
REFERENCE	1 (bases 1 to 839)		
AUTHORS	Bennett,J., Arumugam,K., Laflitte,R., Wen,J., Rudd,S. and Bruskiewich,R.M.		
TITLE	IRRI Drought Stress Panicle cDNA Library		
JOURNAL	Unpublished (2002)		
COMMENT	On Dec 2, 2002 this sequence version replaced gi:25994463.		
FEATURES			
source	Location/Qualifiers		
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	/mol_type="mRNA"		
	/cultivar="IR64"		
	/db_xref="taxon:39946"		
	/clone="C0002165"		
	/isue_type="Panicles"		
	/dev_stage="Flowering"		
	/clone_1ib="IRRI Drought Stress Panicle Library"		
	/notes="Vector: pBluescript II SK+; Water stress was applied by not watering for 4 consecutive days. Panicles were collected from control (well watered) and stressed plants at 2 days before heading, at heading, 50% flowering and 4 days after 50% flowering."		
ORIGIN			
Query Match	31.1%;	Score 395.6;	DB 14; Length 839;
Best Local Similarity	74.4%;	Pred. No. 3.1e-89;	
Matches 511; Conservative	0;	Mismatches 175;	Indels 1; Gaps 1;

QY 441 GTTCTGGAAAAGAAAAAGAACTAGCCGGTTTACCATCGTGTTCAGCATGAG 500
Db 21 GTAATGGAAAAAGAAAAAGAACTAGCTGTGTTAGGCATTGGTGTGTAACATGGA 80
QY 501 TCTGTGAACGTGGCTGTGTGTCATGTTGGCTGGGAATTAGCTTATGGAAAAGAAAC 560
Db 81 AGTGGGGAGCATGACGTGTGCGTGGTGGGAGCTAGGCTATGGAAAAGAAAGGAGC 140
QY 561 TTTTCTTTCCCAATGTTCCACTATGAGCAGACTTTGTAATATGAGTGAAGTATTGGG 620
Db 141 TTTTCATTCCCAATGTTCCCTCCATAGGCAATCTTTATATGAAGTTGAATTTGGG 200
QY 621 TTTGATGAACAAAGAGAGGAAAAGCTCGCATGATATGACTGTATGAGAAAAGATTGGT 680
Db 201 TTTGATGATGTCAAAGAGGAGAAAGCCGGAAGTACATGACATGAGAGAAAGATTGAA 260
QY 681 GCACAGACAGAAAGAAAATGATGGGAATCTCTTTTAAGAGAGAAAAGCTGAGAA 740
Db 261 GCACGGGACAGAGAGAGATGAGGGCAATGATATTTCAAAGAAAAGATTGAGAG 320
QY 741 GCCATGCAACAGTATGAAATGGCCATAGCATATACATGAGGAGCAATTTATGTTTCACTG 800
Db 321 GCCATGCAACAGTATGAAATGGCCATAGCATATGAGGAGCAATTTATGTTTCACTG 380
QY 801 TATGGGAAATGACAGGATATGCTTTAGCACTTAAAGCCATCCATTTTACATGACA 860
Db 381 TTTGGGAAATGACAGGATATGCTTTAGCACTTAAAGCCATCCATTTTACATGACA 440
QY 861 GCTTGGCTTCATCAATCTTAAAGCATATGATGATGAAACATTTGCTCTGCAACA-TTGTGTT 919
Db 441 GCATGGCTTCATCAATCTTAAAGCATATGATGATGAAACATTTGCTCTGCAACA-TTGTGTT 500
QY 920 GACAGAAAGAGAAAAAGCCAAAGCACTGTTCAAGAAAGAGGAAAAGCAAGCAGACT 979
Db 501 GCGAGAGGATTAATTAATGTAAGCACTTTTCAAGAGAGAAAGCAAGCAGTGAAT 560
QY 980 AGGACAGATGAGCTCAGACCTGATGATTTCCGAAAGGACAAAAGTATGCTCTGACA 1039
Db 561 TGCTCAGACAGAAATCAGGAGGAGGAGCACTTCTGAAAGCCAAAGAAATCTCCAGAGA 620
QY 1040 CAAGGCGATTTAGAGAGGCTACAGACCTTGACAGCAAGAGAAAGCTTTGTAACAAA 1099
Db 621 CAAGGAGATCCAGGAGTGGCTTGGCTCTGCGGAAACAGATTAAGCTCTGTAACAAA 680
QY 1100 GCAGAAAGAAATGTACAAAGGATATT 1126
Db 681 ACAGAGAGAGCTGTACNAAGGCTCTT 707

RESULT 10
AM773636 650 bp mRNA linear EST 07-SEP-2000
LOCUS EST133622 KV3 Medicago truncatula cDNA clone pKV3-15123, mRNA
DEFINITION
ACCESSION AM773636
VERSION AM773636
KEYWORDS
SOURCE
ORGANISM
EST.
Medicago truncatula (barrel medic)
Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 650)
Vandenbosch, K., Hutt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
ESTs from roots of Medicago truncatula after Rhizobium inoculation
Unpublished (1999)
Contact: Vandenbosch K
Department of Plant Biology
University of Minnesota
220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA

Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cbs.umn.edu
Texas A&M EST name: T257055e
TIGR sequence name: MTRAM607K
More information is available at:
http://chrysalis.lamu.edu/medicago
Seq primer: Skmod (CTA GAA CTA gta gat CC).
Location/Qualifiers
1..650
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultiivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-15123"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
/lab_host="E. coli strain X10LR"
/clone_lib="KV3"
/note="Vector: Bluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the UniZap XR vector from
stratagene and packaged using gigapack III gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in X10LR cells."

ORIGIN
Query Match 30.8%; Score 391.6; DB 10; Length 650;
Best Local Similarity 75.3%; Pred. No. 3.1e-88;
Matches 487; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
QY 403 TTGAGATATCATGAGCAGAGAGCAACCTATTGATTTGTTCTTGGAAAAGAAAAAG 462
Db 2 TTGAGATATCATGAGCAGAGAGCAACCACTGATGTAATGAGAAAAGAAAAAG 61
QY 463 AACTAGCCGTTTACCATCGTGTGCTAGCATGAGTCTGTGAAGCTGCGCTTGTGC 522
Db 62 AATGACTGGCTTTGGGCACTTGGGGTGGCAAGCATGAAAGCGGGGAGCGAGCATTTTGC 121
QY 523 ATGTGGCTGGGAATTAAGCTTATGAGAAAGAAAGAAACCTTTCTTTCCCATGTTCCAC 582
Db 122 GTGTAGCTGGGAAATTAAGATGATGACAGAGAAAGCACTTTTCATTTCCAAATGTTCCAC 181
QY 583 CTATGAGAGCTGTTATATAGAGTGAAGTATTTGGTGTATGAAAAGAAAGAGAGAA 642
Db 182 CAATGGCAATTTTATGTTATGAGTTGAGCTCATTTGTTTATGTAACAAAGATGGA 241
QY 643 AAGCTCGAGTGAATATGACTGTAGAGAAAGATTTGTCAGAGACAGAGAAAGAAATG 702
Db 242 AAGCTCGAGTGAATATGACTGTAGAGAAAGATTTGTCAGAGACAGAGAAAGATG 301
QY 703 ATGGGAATTTCTTTTAAAGAGAGAAAGCTGAGAGAACATGCAACGATGAATAG 762
Db 302 ATGGAATGTTCTGTTTCAAGAAAATTAACATGAGAGGCCATGCAACGATGAATAG 361
QY 763 CCATACATACATAGGGGAGAGATTTATGTTTACGTGATAGGAAAGTACAGGATATG 822
Db 362 CCATACCTTATATGAGAGATGACTCATGTTTCAAGTTTGGAAAGTATAGGATATG 421
QY 823 CTTTACAGTTTAAAGCCATGCGCATTTTACATAGCAGCTTGCCATCAAACTAAAC 882
Db 422 CTGTGCTGTAAAGATTCATGCACTTAAACAGCGCGGCGCTGTGATTAAGCTGAAC 481
QY 883 GATACATAGAACATTTGCTCACTGCAACATTTGTTGACAGAAAGAGAAAGCCAA 942
Db 482 GCTATGAAGAGATTAAGACATGACATGATTAATGATGAGACGAGCAAAATTTGA 541
QY 943 AAGCAGCTTTCGAAGAGGAAAGCAAGAGCAGAGCTAGAGAGATGAGCTAGCAGCG 1002
Db 542 AGGCTTATTTAGAGAGGATTAAGGCTTAGAGCAGCACTCGGAGAGACAGATGCTMGCCAG 601

Db 108 AAGATGATGAAAATGAAAAGCTATGAGAAAGCTGCGGTGGCTGGAGCTTGGC 167
Qy 244 AAGAGGTTATATGTTCCCTTAAGTTGATGTGAAGCTGAGGCTTGGATGAGAAATCA 303
Db 168 AAGTGGGAATCATCTCTCGAAGTCCGATCCGGGTGTAATCTCTCAAGAGAAATCA 227
Qy 304 GTAAGCAGATTATTAAGAAAGTTCACGGTTCCAAACATCCAGTACTTCAATGCTTTT 363
Db 228 CCAAGCAATATCATTAAGAAAGTTCATGTGAGAACCAACCAATATGCAACATGCTTTT 287
Qy 364 GTCACTACAGGCGATGAGCAAAAATCTGACGACCAAAATTTGAGATACATGCGATAGC 423
Db 288 TGCACTACAGGCGATGAGCAAAAATCTGACGACCAAAATTTGAGATACATGCGATAGC 347
Qy 424 AGCAACCTATTTGATTTGTTCTTCTGAAAAGAAAAGAACTGACGGGTTTAGCCATCG 483
Db 348 AACGACATTTGAAATGTTTATGAAAAGAAAAGAAATGAAATGCGGGTTTAGCTTTG 407
Qy 484 GTGTTGCTAGCATGAGTGTGTGTAAGCTGCGCTTGTGATGTTGCTGGGAATTAGCTT 543
Db 408 GTGTTGCTAGCATGAGTGTGTGTAAGCTGCGCTTGTGATGTTGCTGGGAATTAGCTT 467
Qy 544 ATGGGAAAAGAAAGAACTTTTCTTTTCCCAATGTTCCATGTCGACACTTGTATTATG 603
Db 468 ATGGGAAAAGAAAGAACTTTTCTTTTCCCAATGTTCTCCCATGCGAGATATATATATG 527
Qy 604 AGGTGAAAGTTATGTTGTTGATGAAAAGAAAGGAAAAGCTGCGAGTATGATGCTG 663
Db 528 AAGTCGACTTATGATGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 587
Qy 664 TAGAGAAAGGATTTGTTGCTGACAGACAGAAAGAAATGATGGAATTTCTTTTAAAG 723
Db 588 CAGAGAGAGGATCGGTGACAGACATGAGAAATGATGGAATTTCTTTTAAAG 647
Qy 724 AGGAAAGCTGAGAGAAAGCTGACAGATGATGAAATGCGCATGCTATCATGCGGGA 781
Db 648 AGGAAAGCTGAGAGAGCTATGACAGATGATGAAATGCGCATGATTTTGGCGCA 705

RESULT 13
LOCUS B0994520
DEFINITION B0994520 699 bp mRNA linear EST 21-AUG-2002
Q6F7H10.Y9.ab1 Q6.FRHM lettuce serritola lactuca sativa cDNA clone
Q6F7H10, mRNA sequence.
B0994520
ACCESSION B0994520
VERSION B0994520.1 GI:22414055
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 699)
REFERENCE 1 (bases 1 to 699)
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., Van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compenomics.ucdavis.edu/
TITLE Unpublished (2002)
JOURNAL Contact: Alexander Kozik [R.W.Michelmore]
COMMENT Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Aamundson Hall, UCD, Davis, CA 95616, USA
tel: 1-(530)-742-1742
fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig Q6_CA_contig5377, see http://cgpdb.ucdavis.edu/
for details.
Plate: Q6F7 row: H column: 10.
Location/Qualifiers

source 1..699
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="L.serritola"
/db_xref="taxon:4236"
/clone="Q6F7H10"
/lab_host="E.coli"
/clone_1kb="Q6.FRHM lettuce serritola"
/note="Vector: pBRCDNA5f1ab; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=Q6.FRHM lettuce serritola
TAG_SEQ=CGTTGACGGG"

ORIGIN
Query Match 27.9%; Score 354.4; DB 13; Length 699;
Best Local Similarity 71.4%; Pred. No. 8.3e-79;
Matches 466; Conservative 0; Mismatches 187; Indels 0; Gaps 0;
Qy 474 TTAGCCATCGGTGTTCTAGCATGAAGCTGTGTAACGTCGCTTGTGATGTTGCTG 533
Db 2 TTGGCCATTTGCGCTGAGCTCCATGAAATCGGGGAGCGAGCTGTATCATGTGGTTG 61
Qy 534 GAATTAAGCTTATGGAAGAAAGAACTTTCTTTTCCCAATGTTCCATGTCGACGAC 593
Db 62 GAATTAAGCTTATGGAAGAAAGAACTTTCTTTTCCCAATGTTCCATGTCGACGAC 121
Qy 594 TTGTTATGAGGTTGGAAGTTATGTTGCTTGTGAAACAAAGAGGAAAAGCTGCGAGT 653
Db 122 ATATCTATGAAATGCAATCAATCGGTTTGTGAAACAAAGAGAAAGCTGCTAG 181
Qy 654 GATATGACTGTAGAGAAAGATTTGTTGACGACAGACAGAAAGAAATGATGGAATTTCT 713
Db 182 GATATGACTGTAGAGAAAGATTTGTTGACGACAGACAGAAAGAAATGATGGAATTTCT 241
Qy 714 CTTTATGAGGAGAAAGCTGAGAGAGCCATGCAACAGTGAATGCGCATGCAATAC 773
Db 242 TTGTTCAAGAGAAAGAAATTTAGAGAGGCTATGCAACATATGCAATGCAATGCAATAC 301
Qy 774 ATGGGAGAGATTTTATGTTTTCAGCTGTATGGAAGTATCAAGATATGCTTTAGAGATT 833
Db 302 ATGAATGATGATTTTCAATGTTTCAATTAATGAAAGTATCAAGATATGCTTTAGAGATT 361
Qy 834 AAAAACCATGCGCATTTTAACATAGAGAGCTTGCCTCATCAAACTAAAGATCGATGAA 893
Db 362 AAGAACCTTTGTACCTTAACATAGAGAGCTTGTGATTAAGCTCAAGAGCTATGAGAA 421
Qy 894 GCAATTTGCTACCTGCAACATTTGTTGACAGAGAAAGAGAAAGCCAAAGACATGTTTC 953
Db 422 GCCATTGCTCAAGTGTCTATTTGACTTTGAGAGATCAAAATATGTAAGACATATTTT 481
Qy 954 AGAAGAGGAGAGAGCAAGAGAGCTAGAGACAGATGAGACTGACGACGTGATTTCCGA 1013
Db 482 AGGCGAGGAGAGAGCTGCTGATGAGACTGCGGACAGACGATGCTGCCGAGAGATTTT 541
Qy 1014 AAGGCAAAAAGTATGCTCTGACGACAGAGCGCATTTAGAGAGAGCTAGAGCATTTGCA 1073
Db 542 AAGCGCGTAAATTTTGCCTGTAAGATTAAGCAATTTAGAGAAATTTGGTGTGCTTTAT 601
Qy 1074 GAGCAAGAGAAAGCTTTGTAACAAAGCAAGAAAGAAATGTACAAAGGAATATT 1126
Db 602 GAAGATGATTAAGTTGTTTATGAGAAACAAAGAGAGCTTTATTAAGGCTTGT 654

RESULT 14
BG451848

LOCUS BG451848 667 bp mRNA linear EST 16-MAR-2001
 DEFINITION NP101C01D1P1002 Drought Medicago truncatula cDNA clone NP101C01DT
 5', mRNA sequence.
 ACCESSION BG451848
 VERSION BG451848.1 GI:13370630
 KEYWORDS EST
 SOURCE Medicago truncatula (barrel medic)
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 1 (bases 1 to 667)
 REFERENCE Torres-Jerez, I., Scott, A. D., Harris, A. R., Gonzales, R. A., Bell, C. J.,
 Flores, H. R., Imman, J. T., Weller, J. W. and May, G. D.,
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula drought library
 COMMENT Unpublished (2000)
 CONTACT: May GD
 ORGANISM Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
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 /clone="NP101C01DT"
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 plasmids harvested in a series of days-post-watering
 timepoints."
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 Query Match 26.3%; Score 341.4; DB 12; Length 667;
 Best Local Similarity 78.1%; Pred. NO. 1.6e-75; Indels 1; Gaps 1;
 Matches 422; Conservative 0; Mismatches 117;
 QY 252 AATGTCCTCTAAAGTTAGTGAAGTGAAGTCTTGATGGAAGAAAGTCAAGTAAAGCAG 311
 DB 129 AGTAGTCTCTCAAAAGTTAGTTCTGAAGTTGAAGTTCTTCTATGAAAGCTTACAAACAA 188
 QY 312 ATTATTAAGGAAGGTCACGGTTCACCAACATCCAACTCTACATGCTTTTGTCTACTAC 371
 DB 189 ATTATTAAGGAAGGTCATGCTCAGAAACCTTCCAACTATTCACATCTTCTTCCATTAC 248
 QY 372 AGGCGATGACCAAAACCTGCGACCAATTTTGAAGATACATGCGACGACGACCAACT 431
 DB 249 AGGCGATGCTCTGAGAACACGAGACCAAAATTTGAACATACATGCGACGACGACCA 308
 QY 432 ATTGAATGCTTCTTGGAAGAGAGAAAAAGAACTAGCCGTTAGCCATCGGTTGCT 491
 DB 309 ACTGAGATGCTAATAGAGAAAGAGAAAGAAATGATCTGCTGGCATTTGGGGTGGCA 368
 QY 492 AGCATGAAGTCTGAGAACGTCGCTTGTCATGTTGGCTGGAGATTAGCTTATGGGAAA 551
 DB 369 AGCATGAAGCGGGGAGCGAGCATTTGTCGTGTAGCTGGGAAATTAGATATGACAG 428
 QY 552 GAAGGAAACTTTTCTTCCATATTTCCACTATGCGACAACTTGTATATGAGGGTGA 611
 DB 429 GAAGGAAAGCTTTTCATTTCCAAATGTTCCACCAATGCGCAATTTAGTTATGAGTTGAG 488
 QY 612 GTTATTGGGTTTATGAGAAACAAAGAGGAGAAAGCTGCGAGTATATGACTGTAGAGAA 671
 DB 489 CTGATTGGTTTATGAGAAACAAAGATGAGAAAGCTGCGAGTATATGACTGTAGAGAA 548

QY 672 AGGATTGTCAGACAGACAGAAAGAAATGATGGAAATTTCTTTTATAGAGAGAA 731
 DB 549 CGGATTGGGCGACCGATCGAGAAAGATGATGAAATGTTCTTTTACAGA-AATTA 607
 QY 732 CTGAGGAAGCCATGCAACAGTATGAATGCGCATGATACATGCGGAGCATTTTATG 791
 DB 608 CTAGAGGAGCCATGCGACAGTATGAATGCAATGCTTATATGGAATGACTTCATG 667
 RESULT 15
 LOCUS CF234356 493 bp mRNA linear EST 05-AUG-2003
 DEFINITION PtaJxojxolB9E0909 Poplar cDNA library from young opposite xylem
 Populus alba x Populus tremula cDNA 5', mRNA sequence.
 ACCESSION CF234356
 VERSION CF234356.1 GI:33453785
 KEYWORDS EST
 SOURCE Populus alba x Populus tremula
 ORGANISM Populus alba x Populus tremula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
 1 (bases 1 to 493)
 REFERENCE Dejardin, A., Leple, J.-C., Lesage-Descauses, M.-C., Costa, G. and
 Pilate, G.
 TITLE Expressed sequence tags from poplar tension wood tissues - A
 JOURNAL comparative analysis from multiple libraries
 COMMENT Unpublished (2003)
 CONTACT: Leple JC
 ORGANISM Unit of Forest Improvement, Genetics and Physiology
 National Institute for Agricultural Research (INRA)
 Domaine de Limere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
 Tel: 33 02 38 41 78 00
 Fax: 33 02 38 41 78 79
 Email: Jean-Charles.Lepie@orleans.inra.fr
 PCR Primers
 FORWARD: TriplexA 5' CTCGGAAGCGCGCCATTTGG 3',
 BACKWARD: TriplexA1 5' ATACGACTCATTATGAGGCGA 3',
 Plate: PtaJxojxol row: B column: 9
 Seq primer: TriplexA 5' CTCGGAAGCGCGCCATTTGG 3'.
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 /mol_type="mRNA"
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 /db_xref="taxon:80863"
 /sex="female"
 /tissue_type="Young differentiating xylem harvested on
 opposite wood side of tilted trees"
 /dev_stage="3-years-old poplar trees grown in the nursery"
 /clone_lib="Poplar cDNA library from young opposite xylem"
 /note="A cDNA library was made with mRNA isolated from
 opposite wood tissues corresponding to the differentiating
 xylem collected with a scalpel after debarking the stem.
 The sampling was done on 3 different tilted trees grown in
 the nursery. cDNAs were cloned in an oriented way into
 SfiI (A and B) restriction sites. A one-step conversion of
 Lambda Triplex2 to the corresponding Triplex2 plasmid was
 done via site-specific recombination at loxp sites
 (Clontech; SMART cDNA library construction kit). cDNA
 inserts were PCR amplified using flanking primers and then
 sequenced on a ABI3100 Genetic Analyzer (Applied
 Biosystem)"
 ORIGIN
 Query Match 26.3%; Score 333.4; DB 14; Length 493;
 Best Local Similarity 79.3%; Pred. NO. 1.7e-73; Indels 0; Gaps 0;
 Matches 391; Conservative 0; Mismatches 102;
 QY 477 GCCATGCGTGTGCTGCAATGAAGTCTGAGTGAAGTCTGCTGTCATGTTGCTGGAA 536
 DB 1 GCTGTGTGTTTCCAGTATGAAGGCTGGTGAACGTCCTTTCATCATGTCGCTGGAA 60

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QY 537 TTAGCTTATGGAAAGAAAGAACTTTCTTTCCCAATGTTCCACCTATGGCAGACTTG 596
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QY 597 TTATATGAGGTGGAAGTTATTTGGGTTTGATGAACAAGAGGAAAGCTGCGAGTAT 656
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Db 121 ATATATGAAGTCAGCTTATTTGATTTGAATGAAGTCAAGAAAGGAAAGCTCGTGAT 180
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QY 657 ATGACTGTAGAGAAAGATGTTGTCAGCAGACAGAAAGAAATGATGGGAATTCCTT 716
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Db 181 ATGACTGCAGAAAGAAAGATCGGCGCAGATCGAAAGAAATGGATGGAAATTCCTA 240
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QY 717 TTTAAGAGAGAAACTGAGAAAGCCATGCAACAGTATGAATGGCCATAGCATACATG 776
    |||||
Db 241 TTCAAGAGAGAAAACTTGAGAGGCTATGCAAGCANTATGAATGGCAATTGCATATTG 300
    |||||
QY 777 GGGAGCGATTTTATGTTTCAGCTGTATGGGAAGTACCAAGATATGGCTTTAGCAGTTAA 836
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Db 301 GGTGACGACTTTATGTTTCAGCTGTGTTGGCAAGTACCAAGATATGGCAGTGAAG 360
    |||||
QY 837 AACCCATGCCATCTTAACTATAGCAGCTTGCTCATCAAACTAATAACGATGAAAGCA 896
    |||||
Db 361 AATCCATGTCATCTTAACTATAGCAGCTTGCTCATCAAGCTTGAGGCGCTATGANAAGCC 420
    |||||
QY 897 ATTGTCACCTGCAACATTTGTTGACGAGAGAGAGAAAAACCAAAAGCACTGTCAGA 956
    |||||
Db 421 ATTGCACAATGCAACATTTGTTGTTGANGATGAAGAAACAAATGCTAAGGCTTGTTCAGA 480
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QY 957 AGAGGAAAGCAA 969
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Db 481 ANAGGAAAGCCA 493
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